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	PDB annotation	FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	TRANSCRIPTION REGULATION PROTO- ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC			
	Compound		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;
Table 5	SEQ FOLD score				67.71			87.59
Ta	PMF		0.28	66.0		0.65	0.98	
	Verify score		-0.22	0.53		0.36	0.43	
	Psi Blast		1.2e-10	3.6e-33	3.6e-33	2.4e-27	7.2e-20	2.4e-34
	END		319	446	448	526	531	447
	START		269	366	366	427	474	365
	CHAIN			 A	A	A	⋖	S
	PDB ID		1bor	lalh	laih	lalh	lalh	lmey
	SEQ ID		1117	1118	1118	1118	1118	1118

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	PDB annotation		FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	INCLEIN-DINA INTED ACTION DEOTEIN	DEGIGN 2 CDVCTAI	Officially, a Civil of Automatical Control of Control o	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN
!	Compound		CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTEIN: CHAIN: C F G	1101 ELY, CLEALY: C, 1, C,					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	
Table 5	SEQ	FOLD																															
Tal	PMF	score							1.00							0.95							1.00							0.98			
	Verify	score							0.35							0.29							0.74							99.0			
	Psi	Blast							2.4e-34							1.1e-28							9.6e-21					_		1.2e-09			
		AA							446							527	_						531		-		**			418			
	START	AA			•	_	•		366							422							474							391			
	CHAIN	a							 ပ							ပ		_					ر د				_			 _			
	PDB	a							1mey						1	1mey							1mey		-319			•		1mey			
	SEQ	NÖ E							11118							1118							1118							11118			

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	PDB annotation	DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	FROTEIN-DINA INTERACTION, PROTEIN DESIGN 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGIT ATTOM/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	I I I MAINSCEALF I I OIN	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER PROTFIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2
!	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C E G.	TICOLDIN, CILMIN. C, F, G,		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE: CHAIN:	B, C, E, F;					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;
Table 5	SEQ FOLD					78.42																
Ta	PMF		1.00									0.51							96.0			
	Verify score		0.82									0.22							0.27			
	Psi Blast		8.4e-08			1.2e-41						1.2e-41							3.6e-31			
	END AA.		526			542						531							447			
	START AA		499			365		-				366							366			
	CHAIN		G	,==	_	A						A	_						သ			
	PDB		1mey	<u></u>		1466		•				14f6					_		lubd			
			1118			1118						1118							1118			

	PDB annotation	FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONDNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTTE ZINC ENGED DNA	BINDING DOMAIN	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (ZINC FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	PKOLEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC
	Compound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		SWIS; CHAIN: NULL;		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING
Table 5	SEQ FOLD score											
Ta	PMF		1.00		86.0		0.77		1.00		,	-0.18
	Verify score		0.15		0.05		0.28		80.0			0.08
	Psi Blast		6e-36		0.00036		7.2e-45		1.4e-26			1.7e-17
	END AA		526		418		528		191			80
	START AA		391		393		366		111			22
	CHAIN		ن ن				A		A			V
	PDB ID		lubd		1zfd		2gli		lalh		1	lalh
	SEQ ID NO:		1118		1118		1118		1122			1122

	PDB annotation	FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC	FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC	FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)
	Compound	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	offe, Cirain: B, C,	DNA; CHAIN: A. B. D. E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			
Table 5	SEQ FOLD score																							
Ta	PMF		-0.09		0.48			0.19				1.00							1.00					
	Verify score		-0.00		-0.51			-0.06				0.29							0.25					
	Psi Blast		1.7e-20		2.4e-42			3.4e-23				8.5e-45							3.6e-46					
	END		108	-	472			163				191	_					6	219					,
	START AA		31		363			84				110							158					
	CHAIN ID		Y		A			A				2							ر					
	PDB ID		laih		1a1h			laih	-			1mey	.,					,	Imey			_		
	SEQ B G S		1122		1122			1122				1122						5	7711		***			

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	PDB annotation		COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER AND A)	COMPLEY (7NIC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER, PROTEIN-DNA
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA. CHAM: A B D E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ	FOLD	. -	-										ļ																
Tal	PMF	score	1.00					1	3						1.00			_				1.00							1.00	
	Verify	score	0.25					0.30	()						0.39							0.50							0.50	
	Psi Dleet	Blast	6.8e-46	-				170 17	1:77:1						6.8e-47							6e-51							8.5e-48	
	END V	AA	219	_				747	i t						247							275							275	
	START	AA	138					166	801						166							194							194	
	CHAIN	a	ر ت)						C							၁							C	
	PDB	3	1mey	_				1 more	, incy						1mey			_				lmey							1mey	
	SEQ	NO.	1122					1172	7771						1122							1122						,	1122	

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	PDB annotation	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZNC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score					
Tal	PMF		1.00	1.00	1.00	-0.14
	Verify		0.26	0.20	0.32	0.11
	Psi Blast		1.2e-48	8.5e-50	8.5e-51	3.4e-36
	END		303	331	359	108
1	START AA		222	250	278	30
	CHAIN		U	၁	U	U
	PDB ID		lmey	lmey	Imey	Imey
	SEQ NO:		1122	1122	1122	1122

CHAIN START END Psi Verify PMF SEQ Compound PDB amotation DD AA AB Blast score score Score Score CINC FINGER/DNA) C 306 387 3.46-51 0.53 1.00 DNA; CHAIN: A, B, D, E, COMPLEX (ZINC FINGER) COMPLEX (ZINC FINGER) C 306 388 1.76-51 1.07.33 DNA; CHAIN: A, B, D, E, COMPLEX (ZINC COMPLEX COMPL
Table 5 Tab
HAIN START END Psi Verify PMF D AA Blast score score 306 387 3.4e-51 0.53 1.00 306 388 1.7e-51
HAIN START END Psi Verify PM Blast score score 306 387 3.4e-51 0.53 1.00 306 388 1.7e-51 0.53 1.00 334 415 1.7e-51 0.53 1.00 362 443 1.5e-50 0.13 1.00
HAIN START END Psi Dast AA Blast 306 387 3.4e-51 0 306 388 1.7e-51 334 415 1.7e-51 0 362 443 1.5e-50 0
HAIN START END B AA AA 306 387 306 388 334 415
HAIN START END B AA AA 306 387 306 388 334 415
D D D D D D D D D D D D D D D D D D D
CHAIN
PDB ID Imey Imey Imey Imey Imey
SEQ DO NO: 1122 1122 1122 1122 1122

	PDB annotation	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL
	Compound	PROTBIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score					
Ta	PMF		0.86	1.00	1.00	-0.07
	Verify score		-0.32	80.0	0.21	0.07
	Psi Blast		2.4e-44	1.4e-49	8.5e-33	6.8e-38
	END		499	499	502	135
	START		390	418	446	57
	CHAIN		S	O	C .	S
	PDB		1mey	1mey	1mey	1mey
	SEQ B G ::		1122	1122		1122

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	PDB annotation		STRUCTURE, COMPLEX (ZINC FINGER,DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC
	Compound			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DMA CITABLA B B B	DINA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;
Table 5	SEQ	FOLD								į								_														
Ta	PMF	score		0.81						000	66.0							0.99							1.00							1.00
	Verify	score		0.18						0.65	0.0						1,	0.65							0.0						, ,	0.06
	Psi	Blast		6.8e-41				•		1 20-14	F1-07:1						7	1./6-13						,	1.2e-12	-						7.4e-13
	END:	AA		163						331	1					_	17.1	155			•			007	499						007	
	START	AA		83						304	-						204	50c						470	7/4						777	7/4
	CHAIN	a		<u>-</u>						J.)	-				-															 	
	PDB F	a	-	Imey		_				1mev	_						1 maxi				_			\dagger	ımey						1 mex	7
	SEQ	B Ö	1,00	7711						1122							1122	7711			,			1122							1122	-
								_			_																					_

	PDB annotation	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER
	Compound	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
able 5	SEQ FOLD score				109.62
La	PMF		-0.13	0.77	
	Verify score		0.10	-0.15	
	Psi Blast		1.5e-14	6.8e-35	2.4e-77
	END		104	256	304
	START AA		31	111	138
	CHAIN		V	∢	A
	PDB ID		11f3	1116	1tf6
	SEQ ID NO:		1122	1122	1122

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	PDB annotation		PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2 TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGIT A TION/DNA)	COMPLEX (TRANSCRIPTION	REGIN ATION/DNA) RNA	POLYMER ASE III 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	FOLYMERASE III, 2 TRANSCRIPTION
	Compound			TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;				!	TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S RIBOSOMAI RNA GENE: CHAIN:	BOEF.						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;		
Table 5	SEQ FOLD	score								i				-															
Ta	PMF score			1.00						1.00					_			1.00							96.0				
	Verify score		;	0.01						0.18								-0.07				•		!	-0.17				
	Psi Blast			2.4e-77						3.4e-37								2.4e-74						!	1.2e-75				
	END			331						340								359							415				
	START			139						195	-							195					_		223				
	CHAIN			¥						Ą								Ą							A				
	PDB ID			1476						1tf6								1tf6							1tf6				
	SEQ D	Ö		1122						1122								1122							1122				

	PDB annotation	INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA	POLYMERASE III, 2 TRANSCRIPTION	INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	I KAINSCRIFTION	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGITE ATTON/DNA) RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA POLYMERASE III, 2
	Compound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;			TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN: B. C. E. F:					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;				!	TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;	
Table 5	SEQ FOLD																						
Tal	PMF		0.99				0.72						0.99							1.00			
	Verify score		0.36				-0.20						-0.17							-0.04			
	Psi Blast		6.8e-38				2.4e-72		-				3.4e-37			-				8.5e-37			
	END		459	-			499						481							501			
	START AA		307				307						335					-		363			
	CHAIN		А				A						A			-				A			
	PDB ID		1tf6				1tf6						1tf6							1tf6			
	SEQ ID		1122				1122						1122							1122		_	

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	PDB annotation		TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2 FINGER PROTFIN DNA.	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION
:	Compound			YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA; CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATIOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-
Table 5	SEQ	score																									
Ta	PMF	score		1.00					1.00			-					,	1.00									0.82
	Verify	score		0.18					0.02	•								0.31									-0.19
	Psi Dlact	Diast		4.8e-58					1.7e-32									1.7e-32				_					2.4e-57
	END	AA		247					247						•		, ,	275									331
	START	AA		137					141								1	174									193
	CHAIN	3		ن ک	1.00				C					-													C
	PDB II	3		1ubd					lubd		_						-	lubd	_								Inbd
	SEQ ==	NO.		1122					1122								,	1122									1122

!	PDB annotation	REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2
	Compound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD score				
Tal	PMF		1.00	1.00	1.00
	Verify		-0.09	0.11	0.19
	Psi Blast		le-33	3.46-35	3.4e-36
	END		303	331	359
	START AA		202	230	258
	CHAIN		U	C	ပ
	PDB ID		1ubd	lubd	1ubd
	SEQ NO:		1122	1122	1122

Table 5 Table 5				·,·																			
Table 5 Table 5 Table 5 Table 5 Table 5 Table 5 Table 6 Table 6 Table 6 Table 7 Table 6 Table 6 Table 7 Table 6 Table 6 Table 7 Table 7 Table 7 Table 7 Table 8 Table 7 Table 8 Table 8 Table 8 Table 8 Table 9 Tabl		PDB annotation	FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONDNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA- PROTEIN RECOGNITION. 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	PEGIT ATTON/DNA) VING	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) YING- VANG 1: TRANSCRIPTION	INITIATION INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION REGULATIONDNA)
PDB CHAIN START END Psi Verify PMF		Compound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;			VXVI. CITARI O. ADENIO	I I; CHAIN: C; ADEINO- ASSOCIATED VIRIS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					CARROLL CARREST AND PARKS	YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS INITIATOR FLEMENT DNA:	CHAIN: A. B.				
PDB CHAIN START END Psi Verify PM Inbd C 281 388 9.6e-55 -0.35 0.69 Iubd C 283 415 9.6e-55 -0.35 0.69 Iubd C 286 387 1.7e-35 0.16 1.00	ble 5	SEQ FOLD score		94.96																			
PDB CHAIN START END Psi ID AA AA Blast Iubd C 281 388 9.6e-55 Iubd C 283 415 9.6e-55 Iubd C 283 415 9.6e-55 Iubd C 283 415 9.6e-55	Та	PMF score						07.0	0.03							30	00.1						
PDB CHAIN START END		Verify						0.25	-0.33							,,,	0.16						
PDB CHAIN START D D AA lubd C 281 3 lubd C 283 4 lubd C 286 3		Psi Blast		9.6e-55	-			0 60 55	7.00-7.7							1 2 2	1./e-35						
PDB CHAIN D D Iubd C Iubd C		END		388				415	t -							200	787						
PDB D D Iubbd O Iubbd O Iubbd O		START		281				202	C07							700	987						
		CHAIN	į	ပ					٠								ر-				-		!
- 1		PDB		lubd				\top								\top		*****		<u> </u>			
0 4 1		SEQ B G Si		1122				1177	7711							1100	7711	_					

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	ion	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG I; TRANSCRIPTION INITIATION, INITIATOR
	PDB annotation	COMPLEX (TRANSCRIPTIC REGULATIONDNA) YING YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTIC REGULATION/DNA)	COMPLEX (TRANSCRIPTEGULATION/DNA) YIN YANG 1; TRANSCRIPTIC INITIATION, INITIATIOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNAPROTEIN RECOGNITION COMPLEX (TRANSCRIPTEGULATION/DNA)	COMPLEX (TRANSCRIP) REGULATION/DNA) YIN YANG 1; TRANSCRIPTIC INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION COMPLEX (TRANSCRIP) REGULATION/DNA)	COMPLEX (TRANSCRIP REGULATION/DNA) YIN YANG I; TRANSCRIPTIC INITIATION, INITIATOR
	PDB	APLEX (HULATIC MG 1; TR TATION MENT, JER PROTEIN RI APLEX (HULATIC	APLEX (MULATIC MG 1; TR TATION MENT, SER PRO TEIN RI	APLEX (FULATION TATION	APLEX (FULATION SG 1; TR
}		REG YAN YAN INIT ELE FINC PRO COM	CON REG YAN INIT ELE FINC PRO CON	CON REC YAN INIT ELE FING PRC CON	CON
	Compound	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD				
Ta	PMF	-0.15	1.00	0.63	0.93
	Verify score	0.22	0.25	-0.35	-0.22
	Psi Blast	3.4e-24	3.4e-35	2.4e-54	1.7e-34
	END AA	135	443	499	499
	START AA	33	342	360	398
	CHAIN	O	O	O	၁
	PDB	1ubd	lubd	lubd	1ubd
	SEQ EL SE	1122	1122	1122	1122

	PDB annotation		ELEMENT, YY1, ZINC 2 FINGER PROTEIN. DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	KEGULA HON/DNA) YING-	INITIATION INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC
	Compound	!					YY1; CHAIN: C; ADENO-	ASSOCIATED VINOS FO	CHAIN: A. B:						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;	
Table 5	SEQ	FOLD																											-		
Ta	PMF	score					0.07								0.64									1.00					0.81		
	Verify	score					-0.18								0.07									-0.02					-0.20		
	Psi	Blast					8.5e-27								3.4e-31								;	3.6e-60					1.2e-75		
	END:	AA					163								191									276					333		
	START	AA					09								98							_		130	-				138		
	CHAIN	a					ပ			-					ပ	_			_					A					A		
}	PDB	a					lubd			•					lubd		•				-		:	2glı					2gli		
	SEQ	a ÿ					122								1122						_		9	7711					1122		

F							$\overline{}$				\neg																			٦
	PDB annotation	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGEK, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI, GLI, ZINC FINGER, COMPLEX (DNA-	
	Compound		ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		
Table 5	SEQ FOLD score						99.38												-				-							
Tal	PMF		1.00									1.00					1.00					1.00					1.00			
	Verify score		90.0									-0.05				!	0.57					0.31					0.17			
	Psi Blast		1.2e-33				7.2e-70					7.2e-70					3.4e-34					5.1e-34					1.5e-33			
	END		330				389					473					442	•				470					498			
	START AA		202				250					306					314			_		342					370			1
	CHAIN		A				A					А					A					A	·				А			J
	PDB ID		2gli				2gli					2gli					2gli					2gli		_			2gli			
	S B B B B		1122				1122					1122					1122		_			1122					1122			

	PDB annotation	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	AMINOACYL-TRNA SYNTHETASE METRS; AMINOACYL-TRNA	SYNTHETASE, ROSSMANN FOLD	AMINOACYL-TRNA SYNTHASE	AMINOACYL-TRNA	SYNTHASE	COMPLEX (TRNA SYNTHETASE/TRNA)	GLNRS; TRNA	SYNTHETANE, GLUTAMINE, TRNAGLN, E. COLI, COMPLEX	COMPLEX (TRNA SYNTHETASE/TRNA)	GLNRS; TRNA SYNTHETASE, GLUTAMINE, TRNAGI'N F. COLI	COMPLEX	
	Compound		ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	METHIONYL-TRNA SYNTHETASE; CHAIN: NULL;		GLUTAMYL-TRNA SYNTHETASE; 1GLN 4 CHAIN: NULL 1GLN 5	GLUTAMYL-TRNA	SYNTHETASE; 1GLN 4 CHAIN: NULL 1GLN 5	GLUTAMINYL-TRNA SYNTHETASE; CHAIN: A: TRNA	GLN II; CHAIN: B;		GLUTAMINYL-TRNA SYNTHETASE; CHAIN: A; TRNA	GLN II; CHAIN: B;		
Table 5	SEQ FOLD score			70.99		340.16			109.90						
Tal	PMF		0.83				1.00					0.40			
	Verify score		0.31				0.53					-0.05			
	Psi Blast		3.4e-31	1.7e-46		le-76	1e-76		6.8e-52			6.8e-52			
	END		218	523		522	522		523			495			
	START AA		83	37		36	37		18			23			
	CHAIN		∀						A.			A			
	PDB ID		2gli	1a8h		1gln	1gh		1qtq		-	1qtq			
	SEQ El Si		1122	1124		1124	1124		1124			1124			

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	PDB annotation	COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA- BINDING PROTEIN 1PDN 14	COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA- BINDING PROTEIN 1PDN 14	COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA- BINDING PROTEIN 1PDN 14	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN- DNA INTERACTIONS, 2 GENE REGULATION/DNA	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN- DNA INTERACTIONS, 2 GENE REGULATION/DNA	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN- DNA INTERACTIONS, 2 GENE REGULATION/DNA	
	Compound	PRD PAIRED DOMAIN; CHAIN: C; 1PDN 4 DNA; CHAIN: A, B 1PDN 5	PRD PAIRED DOMAIN; CHAIN: C; IPDN 4 DNA; CHAIN: A, B IPDN 5	PRD PAIRED DOMAIN; CHAIN: C; 1PDN 4 DNA; CHAIN: A, B 1PDN 5	HOMEOBOX PROTEIN PAX-6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	HOMEOBOX PROTEIN PAX-6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	HOMEOBOX PROTEIN PAX-6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	
Table 5	SEQ FOLD score		169.42		165.42			
Ta	PMF	1.00		1.00		1.00	1.00	
	Verify score	0.45		89.0		0.50	0.42	
	Psi Blast	5.1e-34	6.6e-65	6.6e-65	1.1e-70	1.1e-70	5.1e-39	
	END	195	197	197	206	206	206	
	START	75	75	76	74	74	75	
	CHAIN	O .	O.	C	A	A	¥	
	PDB ID	1pdn	Ipdn	lpd1	брах	брах	брах	
	N 6 6	1128	1128	1128	1128	1128	1128	

	PDB annotation		HYDROLASE TETRATRICOPEPTIDE, TRP:	HYDROLASE,	PHOSPHATASE, PROTEIN-	PROTEIN INTERACTIONS,	TPR, 2 SUPER-HELIX, X-RAY Striictire	TRANSFERASE ATK,	AMGX1, BPK; TYROSINE	KINASE, X-LINKED	AGAMMAGLOBULINEMIA,	XLA, BTK, SH3 2 DOMAIN,	TRANSFERASE	COMPLEX	(TRANSFERASE/PEPTIDE)	(TP A NISEED A SE (DEDITINE)	CICHAI TO ANCOLICATION 2	SIGNAL I KANSDUCIION, 2 SH3 DOMAIN											TRANSFERASE PROTO-	ONCOGENE TYROSINE
	Compound		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;					BRUTON'S TYROSINE KINASE;	CHAIN: NULL;				TO THE MENON THE PARTY OF THE PARTY AND THE	ABL I KOSINE KINASE; CHAIN:	A, C, E, G; PEPTIDE P41; CHAIN: B. D. F. H:				COMPLEX (ONCOGENE	PROTEIN/PEPTIDE) C-CRK (N-	TERMINAL SH3 DOMAIN) (C-	CRKSH3-N) COMPLEXED WITH	1CKA 3 C3G PEPTIDE (PRO-PRO-	PRO-ALA-LEU-PRO-PRO-LYS-	LYS-ARG) 1CKA 4	PHOSPHOTRANSFERASE C-SRC	KINASE (SH3 DOMAIN)	(E.C.2.7.1.112) 1CSK 3	PHOSPHOTRANSFERASE FYN;	CHAIN: A; 3BP-2; CHAIN: B;
Table 5	SEQ	FOLD score																												
Te	PMF	score	0.04					0.76					700	40.0					0.34							0.62			0.22	
	Verify	score	-0.41					0.05					0.00	67.0					0.05							1.01			0.21	
	Psi	Blast	0.00084					2.4e-07					0 60 00	7.00-					7.2e-08							7.2e-08			1.2e-07	_
	END:	AA	1378					64					89	3					64							29			89	
	START	AA	1270					4					14	-					14										14	
	CHAIN	CII											A	4	_				A	_						A			A	
	PDB	≘	1a17					laww					1hhz			_			1cka							Icsk		,	1tyn	
	SEQ	S E	1132					1132					1132						1132						+	1132			1132	
																_		_	_			_			_		_			_

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	PDB annotation		KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN	KINASE, 2 PHOSPHORYI. ATION ATP.	BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX	(PHOSPHOTRANSFERASE/PE PTIDE)		TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE		PATHOGENESIS-RELATED PROTEIN PATHOGENESIS- RELATED LEAF PROTEIN 6,	ETHYLENE PATHOGENESIS- RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-	RELATED LEAF PROTEIN 6,	ETHYLENE PATHOGENESIS- RELATED PROTEIN, PR-1
	Compound	,					PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	HEMATOPOIETIC CELL KINASE; CHAIN: NULL;		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;		
Table 5	SEQ FOLD	score				!				52.74				
Та	PMF						99.0	0.22				1.00		
	Verify score						0.33	0.12				0.52		
	Psi Blast					_	2.4e-07	1.2e-08		1.7e-38		1.7e-38		
	END						68	89		119		119		
	START AA						14	10		7		7		
	CHAIN			-			А							
	PDB ID						1shf	4hck		1cfe		1cfe		
	SEQ E	SO.					1132	1132		1137		1137		

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	PDB annotation	PROTEINS, 2 PLANT DEFENSE	ALLERGEN ANTIGEN 5; ANTIGEN 5, ALLERGEN, VESPID VENOM		COMPLEX (INHIBITOR/NUCLEASE) COMPLEX	(INHIBITOR/NUCLEASE), COMPLEX (RI-ANG),	HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE	MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX	(INHIBITOR/NUCLEASE)	(INHIBITOR/NUCLEASE),	COMPLEX (RI-ANG),	HYDROLASE 2 MOLECULAR	RECOGNITION, EPITOPE	MAPPING, LEUCINE-RICH 3	REPEATS	(INHIBITOR ANTICTER SE)	COMPLEX	(INHIBITOR/NUCLEASE),	COMPLEX (RI-ANG),	HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE
	Compound		VES V 5; CHAIN: A;		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;				RIBONUCLEASE INHIBITOR;	CHAIN: A, D; ANGIOGENIN; CHAIN: B F:						TOTAL COLUMNICATION OF THE PROPERTY OF THE PRO	KIBOINOCLEASE INFIBITOR; CHAIN: A. D. ANGIOGENIN:	CHAIN: B, E;			
Table 5	SEQ FOLD score																				
Ta	PMF		66.0		0.05			-	69.0							000	0.0				
	Verify score		0.44		-0.21				0.54							0.07	``. ``.				
	Psi Blast		1.7e-29		1.7e-10				ee-07							6 84 06	200				
	END		122		286				303							308					
	START AA				124				183	12.00		=				212	 				
	CHAIN		A		V				~_ &		A										
200	PDB ID		lqmx		la4y			,	la4y							la4v					
0	S B S		1137	1120	1138				1138							1138					

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	PDB annotation	MAPPING, LEUCINE-RICH 3 REPEATS	CELL ADHESION LEUCINE	RICH REFEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSF	EKASE, 2.0 A 2	RESOLUTION, N-	FORMYLMETHIONINE,	ALPHA SUBUNIT, BETA	SUBUNIT		GUANINE NUCLEOTIDE	EXCHANGE FACTOR RCC1;	GUANINE NUCLEOTIDE	EXCHANGE FACTOR, GEF,	RAN, 2 RAS-LIKE NUCLEAR	GTP RINDING PROTEIN	HEADER TER	GUANINE NUCLEOTIDE	EXCHANGE FACTOR RCC1:	GUANINE NUCLEOTIDE	EXCHANGE FACTOR GEF	RAN 2 RAS-1 IKE MICI BAR	GTP BINDING PROTEIN	HEADER TER	HEADEN LEN	COMPLEX (BLOOD COAGULATION/INHIBITOR)	
	Compound		INTERNALIN B; CHAIN: A;		RAB	GERANYLGERANYLTRANSFER	ASE ALPHA SUBUNIT; CHAIN:	A, C; KAB	GERANYLGERANYLTRANSFER	ASE BETA SUBUNIT; CHAIN: B,	D;		many and the state of the state	REGULATOR OF CHROMOSOME	CONDENSATION 1; CHAIN: A, B,	౮					REGULATOR OF CHROMOSOME	CONDENSATION 1: CHAIN: A. B.	C						FACTOR IXA; CHAIN: C, L,; D-PHE-PRO-ARG; CHAIN: I;	
Table 5	SEQ FOLD score	, .												00.06																
Tal	PMF		0.04		0.01																0.93								90.0	
	Verify score		-0.34		-0.27																0.50								-0.15	
	Psi Blast		6.8e-19		1e-08								,	1.4e-63							1.4e-63			•					0.0006	
	END		308		308								\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	376							376								280	
	START AA		165		198									_						_	20		_						236	
	CHAIN		A		A									A	-		-				A			-					T	
	PDB ID		140b		1dce		_	-					,	lal2			•				la12								Ipfx	
	SEQ ID NO:		1138		1138								;	1141							1141								1145	

	PDB annotation	CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT ANK REPEAT	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION
	Compound		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E; GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA;
Table 5	SEQ FOLD	71076				
Tal	PMF		0.94	0.98		0.95
	Verify score		0.81	0.40		0.32
	Psi Blast		3.4e-21	4.8e-30	0	3.4e-38
	END AA		969	629		663
	START AA		581	482	C	508
	CHAIN			В	ļ	В
	PDB ID		1a5e	lawc		lawc
	S E E E	5	1148	1148	07	1148

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	PDB annotation	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANK YRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION BECITTA ATTOMISMA)	GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA- BINDING, 2 NUCLEAR	PROTEIN, ETS DOMAIN,	TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR	TUMOR SUPPRESSOR,	CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR	TUMOR SUPPRESSOR,	CDK4/6 INHIBITOR,	TUMOR SUPPRESSOR	TUMOR SUPPRESSOR,	CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR, TUMOR SUPPRESSOR,
	Compound	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A: GA BINDING	PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	\ \ \			P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;			P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;
Table 5	SEQ FOLD score																	
Tat	PMF		1.00					86.0			1.00			1.00				0.99
	Verify		0.74					0.26			99.0			0.56				0.43
	Ps1 Blast		8.5e-38					8.5e-26	-		1.2e-36			3.4e-33				1e-27
1	END		969					599			<i>L</i> 99		-	999				669
	SIAKI AA		542					451			504		-	511				545
	CHAIN		В															
	PDB TD		1awc	· · · · · ·				1bd8			1bd8			1bd8	<u> </u>			1bd8
000	NO EX		1148					1148			1148			1148				1148

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	PDB annotation		CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6;	P16INK4A, MTS1; CYCLIN	DEPENDENT KINASE, CYCLIN DEPENDENT	KINASE INHIBITORY 2	PROTEIN, CDK, INK4, CELL	CYCLE, MULTIPLE TUMOR	SUPPRESSOR, 3 MTS1,	COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	COMPLEX (KINASE/ANTI-	ONCOGENE) CDK6;	P16INK4A, MTS1; CYCLIN	DEPENDENT KINASE,	CYCLIN DEPENDENT	KINASE INHIBITORY 2	PROTEIN, CDK, INK4, CELL	CYCLE, MULTIPLE TUMOR	SUPPRESSOR, 3 MTS1,	COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	COMPLEX (INHIBITOR	PROTEIN/KINASE)	INHIBITOR PROTEIN,	CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2	CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR
	Compound			CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR	SUPPRESSOR; CHAIN: B;								CYCLIN-DEPENDENT KINASE 6;	CHAIN: A; MULTIPLE TUMOR	SUPPRESSOR; CHAIN: B;									CYCLIN-DEPENDENT KINASE 6;	CHAIN: A; P19INK4D; CHAIN: B;				
Table 5	SEQ	FOLD score																											
Ta	PMF	score		96.0								1	0.98											0.99					
	Verify	score		0.73	_				_				0.70									_		0.33					
	Psi	Blast		3.6e-25	_								5.1e-22											6.8e-27					
	END	AA		630								, ,	969										,	669					
	START	AA		504								,	180											545					
	CHAIN	a		В								1	a						-					<u>a</u>					
	PDB	a │		1bi7			140				wu	;	lb1/						-					lblx		_			-5 v.,
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	PDB annotation	PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIRITOR	PISINK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH	FACTOR	HORMONE/GROWTH FACTOR P18-INK4C: CELL	CYCLE INHIBITOR,	P18INK4C, TUMOR,	SUPPRESSOR, CYCLIN- 2	DEPENDENT KINASE,	HORMONE/GROWTH	FACTOR	HORMONE/GROWTH	FACTOR P18-INK4C; CELL	CYCLE INHIBITOR,	P18INK4C, TUMOR,	SUPPRESSOR, CYCLIN-2	DEPENDENT KINASE,	HORMONE/GROWTH	FACTOR	HORMONE/GROWTH	FACTOR P18-INK4C; CELL	CYCLE INHIBITOR,	P18INK4C, TUMOR,	SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE	
	Compound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;			CYCLIN-DEPENDENT KINASE 6 INHIBITOR: CHAIN: A:							CYCLIN-DEPENDENT KINASE 6	INHIBITOR; CHAIN: A;							CYCLIN-DEPENDENT KINASE 6	INHIBITOR; CHAIN: A;				
Table 5	SEQ FOLD	SCOLC																								
Ta	PMF		0.23			0.95							0.25								0.58					
	Verify score		0.19		,	29.0							0.47								0.83					
	Psi Blast		5.1e-25			3.4e-28							1.7e-36								3.4e-34					
	END		998		<u>-</u> '	628							899								701					7
	START AA		425			474							508								555					
	CHAIN		A			A							A								A					
	PDB ID		1bu9		_	1bu9							1bu9								1bu9					
!	SEQ ED SEQ		1148			1148							1148			•					1148					

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	PDB annotation	HORMONE/GROWTH FACTOR	STRUCTURAL PROTEIN TWO REPEATS OF	SPECTRIN, ALPHA HELICAL	TANDEM 3-HELIX COILED-	COILS, STRUCTURAL PROTEIN	SIGNALING PROTEIN	HELLA-TUKN-HELLA, ANKYRIN REPEAT	SIGNALING PROTEIN	HELIX-TURN-HELIX,	ANKYRIN REPEAT	METAL BINDING PROTEIN	ZINC-BINDING MODULE,	ANKYRIN REPEATS, METAL	BINDING PROTEIN	CELL CYCLE INHIBITOR	P18-INK4C(INK6); CELL	CYCLE INHIBITOR, P18-	INK4C(INK6), ANKYRIN	REPEAT, 2 CDK 4/6	INHIBITOR	CELL CYCLE INHIBITOR	P18-INK4C(INK6); CELL	CYCLE INHIBITOR, P18-	INK4C(INK6), ANKYRIN	REPEAT, 2 CDK 4/6 INHIBITOR	
	Compound		ALPHA SPECTRIN; CHAIN: A, B, C;				CYCLIN-DEPENDENT KINASE 4	INFIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4	INHIBITOR B; CHAIN: A;		PYK2-ASSOCIATED PROTEIN	BETA; CHAIN: A;			CYCLIN-DEPENDENT KINASE 6	INHIBITOR; CHAIN: A, B;					CYCLIN-DEPENDENT KINASE 6	INHIBITOR; CHAIN: A, B;				
Table 5	SEQ FOLD score																										
Tal	PMF		0.36				0.82		09.0			0.62				1.00						1.00					
	Verify score		0.15				0.49		06.0			0.56				0.56						0.56					
	Psi Blast		3.6e-05				2.4e-32		5.1e-22			6.8e-17				3.4e-28		_	-			8.5e-36					
ļ	END		285				636		969			669				628			•			299					
	START		89				497		581			612				474						508				ŀ	
	CHAIN ID	!	A				A		A			A				А						A		_			
	PDB ID		1cun				1d9s		1d9s			1dcq				1ihb						1ihb					
!	SEQ ID NO:		1148				1148		1148			1148				1148						1148					

	PDB annotation	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65, P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION
	Compound	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B- ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B- ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;
Table 5	SEQ FOLD score							
Tal	PMF	96.0	0.00	1.00	69:0	0.15	0.00	1.00
	Verify score	0.82	-0.09	0.65	0.43	0.20	-0.03	0.67
ļ	Psi Blast	1.7e-33	5.1e-29	1.7e-39	3.4e-24	1.2e-17	1.7e-29	3.4e-39
	END	700	580	969	969	701	580	969
	START AA	555	434	503	582	615	427	502
	CHAIN	A	D	D	_		ш	Щ
	PDB ID	1inb	likn	likn	lmyo	1myo	lnfi	lnfi
!	SEQ ID NO:	1148	1148	1148	1148	1148	1148	1148

	PDB annotation	REGULATION/ANK	REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (ANTI-	ONCOGENE/ANKYRIN	REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR	SUPPRESSOR, MULTIGENE 2	FAMILY, NUCLEAR	PROTEIN,	PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX	(ANTI-	ONCOGENE/ANKYRIN	REPEATS)	COMPLEX (ANTI-	ONCOGENE/ANKYRIN	REPEATS) P53BP2; ANKYRIN	REPEATS, SH3, P53, TUMOR	SUPPRESSOR, MULIIGENE 2	FAMILY, NUCLEAR	PROTEIN,	PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX	(ANTI-	ONCOGENE/ANKYRIN	REPEATS)	LIM DOMAIN CONTAINING
	Compound			P53; CHAIN: A; 53BP2; CHAIN: B;												P53; CHAIN: A; 53BP2; CHAIN: B;													QCRP2 (LIM1); CHAIN: NULL;
Table 5	SEQ FOLD	score																											
Ta	PMF score			1.00												0.09													0.63
	Verify score			29.0												0.36													0.35
	Psi Blast			6.8e-19												1.7e-19		•											2.4e-12
	END			969												701													221
	START AA			581												989									-				162
	CHAIN			В												B													
	PDB			1ycs												1ycs													1a7i
	S B B	S.		1148												1148													1153

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	PDB annotation	PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN- BINDING DOMAIN, CYTOSKELETON	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN- BINDING DOMAIN, CYTOSKELETON	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR
	Compound		CRP1; CHAIN: A;	UTROPHIN; CHAIN: A, B;	SPECTRIN BETA CHAIN; CHAIN: A;	SPECTRIN BETA CHAIN; CHAIN: A;	AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	DYSTROPHIN; CHAIN: A, B, C, D;
Table 5	SEQ FOLD score				104.59				
Tal	PMF		0.71	1.00		1.00	96.0	69:0	1.00
	Verify		0.54	0.76		0.82	69.0	0.58	0.84
:	Psi Blast		6e-12	1.4e-36	6.8e-47	6.8e-47	1.2e-10	2.4e-11	5.1e-37
	END		217	105	110	110	217	220	110
	START AA		155	5	2	4	161	161	5
	CHAIN		A	A	¥	₩.		A	A
	PDB		1b8t	1bhd	16kr	16kr	lctl	1cxx	1dxx
	SEQ NO.		1153	1153	1153	1153	1153	1153	1153

	PDB annotation	DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN-BINDING, UTROPHIN	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING ACTIN BINDING	2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN	METAL-BINDING PROTEIN LIM DOMAIN, ZINC-FINGER, METAL-BINDING PROTEIN	TRANSFERASE PYROCOCCUS FURIOSUS, HYPERTHERMOPHILES, ADP SITE, 2 PHOSPHORYL GROUP TRANSFER, ARGININE METABOLISM	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE	PROTEIN, REGULATORY, CALCIUM BINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE	PROTEIN, REGULATORY, CALCIUM BINDING	MUSCLE PROTEIN CTNC,	CARDIAC, MUSCLE PROTEIN, REGULATORY,
	Compound		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;		LASP-1; CHAIN: NULL;	CARBAMATE KINASE-LIKE CARBAMOYLPHOSPHATE SYNTHETASE; CHAIN: A;	TROPONIN C; CHAIN: NULL;		TROPONIN C; CHAIN: NULL;		TROPONIN C; CHAIN: NULL;	
Table 5	SEQ FOLD score						57.30					
Ta	PMF score		1.00		0.49	0.09			0.59		0.54	
	Verify score	!	0.64		-0.45	-0.37			~0.00		0.25	
	Psi Blast		3.4e-37		4.8e-05	1.7e-33	1.7e-44		1.7e-44		1.7e-42	
	END		109		189	207	273		270		350	
	START		5		161	=	102		110		198	
	CHAIN		A			A						
	PDB ID		1qag		1zfo	1619	1aj4 		laj4		laj4	
	SEQ NO:	- 1 7 7	1153		1153	1155	1156		1156		1156	

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	PDB annotation	CALCIUM BINDING	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE	IMMUNOSUPPRESSION																	
	Compound		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF ICDM 3	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODOLIN-BINDING	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	1CLL 3	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	1CLL 3	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)
Table 5	SEQ FOLD	score				-													56.73		
Ta	PMF		0.70		0.99			0.99				0.00					0.99				0.84
	Score 0.06				-0.05	0.14	-0.17					0.31				-0.10					
ļ	Psi Blast		1.5e-34		3.4e-53		8.5e-52	1.2e-28					5.1e-58		6.8e-56		6.8e-56				
!	END		355	270		346	371					270		348		346					
	START AA 203				112	112						280					112		196		201
	CHAIN ID B A A							A				A					j				
!	PDB ID		1aui	1cdm	1cdm	1cdm					lcli		1cII		1cll						
	SEQ ID	NO:	1156		1156			1156				1156					1156		1156		1156

	PDB annotation					CALCIUM-BINDING	PROTEIN CALMODULIN APO TR2C-DOMAIN: 1CM	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN	HELIX-TURN-HELIX	METAL TRANSPORT	CALMODULIN, HIGH	RESOLUTION, DISORDER	METAL TRANSPORT	CALMODULIN, HIGH	RESOLUTION, DISORDER	TRANSPORT PROTEIN	CALCIUM BINDING, EF	HAND, FOUR-HELIX	BUNDLE	CALCIUM-REGULATED	MUSCLE CONTRACTION	MUSCLE CONTRACTION,	CALCIUM-BINDING,	TROPONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN,	CALCIUM-REGULATED 3	MUSCLE CONTRACTION	CALCIUM-REGULATED
	Compound			1CLL 3	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	CALMODULIN (VERTEBRATE);	ICMF 6 CHAIN: NULL; 1CMF 7	CARDIAC TROPONIN C; CHAIN:	CARDIAC TROPONIN C: CHAIN:	A;	CALMODULIN; CHAIN: A;			CALMODULIN; CHAIN: A;			CALMODULIN; CHAIN: A;				TROPONIN C; CHAIN: NULL;									TROPONIN C; CHAIN: NULL;
Table 5	SEQ	FOLD	score														_													59.86
Te	PMF				0.11	0.72		1.00	0.98	0.98		96.0		0.86			1.00				0.94									
	Verify	score	ļ		0.03	0.11		0.14	-0.07		0.31			0.16			0.31				0.26									
	Psi	Blast 6.8e-29			6.8e-29	3.4e-30			3.4e-38		3.4e-56			1.7e-54			1.4e-29				3.4e-48									3.4e-45
	ONG ;	ΑA			371	346		270	349		271			346			346				769									347
	START	AA			280	278		110	198		110			198			283			00,	109									194
	CHAIN	∄						¥	A		Ą			А			A													
	PDB	₽			1cli	1cmf		1dtl	1dtl		1exr			lexr			1171	_			1101			_					,	ltcf
	SEQ E	3 5	SC.		1156	1156		1156	1156		1156		,	1156			1156			1150	0001								,	1156

PDB annotation	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3	CALCTUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCTUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCTUM-REGULATED 3	CALCIUM-BINDING PROTEIN EF HAND 17532 14	CALCIUM-BINDING PROTEIN EF-HAND (TNX 14	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14	CALCIUM-BINDING PROTEIN EE-HAND 1TNX 14	+1 VVIII (VVIII) - 17 VVIII (VVIII)		
Compound		TROPONIN C; CHAIN: NULL;	TROPONIN C; 1TNX 4 CHAIN: NIII I: 1TNX 5	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	TROPONIN C; 1TNX 4 CHAIN: NULL: 1TNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 170P 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 170P 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3
SEQ FOLD				55.58					57.55
PMF		0.86	0.70		1.00	0.03	1.00	0.77	
Verify		-0.01	-0.15		0.15	0.00	0.19	0.26	
Psi Blast		3.4e-45	8.5e-46	1.5e-41	1.5e-41	3.4e-26	5.1e-49	6.8e-46	5.1e-49
END AA		346	269	346	346	371	269	350	273
START		201	111	194	199	279	111	199	66
CHAIN									
PDB ED		ltcf	1tmx	1tmx	1tmx	1tmx	1top	ltop	1top
A B B		1156	1156	1156	1156			- $+$	1156
	PDB CHAIN START END Psi Verify PMF SEQ Compound ID ID AA AA Blast score score FOLD	PDB CHAIN START END Psi Verify PMF SEQ Compound ID D AA AA Blast score FOLD score Score ROLD Score Scor	PDB CHAIN START END Psi Verify PMF SEQ Compound D AA AB Blast score score FOLD score 1	PDB	PDB CHAIN START END Psi Verify PMF SEQ Compound	PDB CHAIN START END	PDB CHAIN START END Psi Verify PMF SEQ Score FOLD	PDB CHAIN START END Psi Verify PMF Score FOLD	PDB CHAIN START EMD Psi Verify PMF SEQ Score Score

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	PDB annotation		CALMODULIN, CALCIUM BINDING, HELIX-LOOP- HELIX, SIGNALLING, 2 COMPLEX(CALCIUM- BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP- HELIX, SIGNALLING, 2 COMPLEX(CALCIUM- BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP- HELIX, SIGNALLING, 2 COMPLEX(CALCIUM- BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP- HELIX, SIGNALLING, 2 COMPLEX(CALCIUM- BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP- HELIX, SIGNALLING, 2 COMPLEX(CALCIUM- BINDING PROTEIN/PEPTIDE)
	Compound	CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	CALMODULIN; CHAIN: A; RS20; CHAIN: B;				
Table 5	SEQ FOLD score			56.98			
Ta	PMF	89.0	0.94		66.0	-0.17	0.17
	Verify score	-0.24	0.01		0.20	0.03	0.13
	Psi Blast	1e-29	8.5e-57	8.5e-57	3.4e-55	8.5e-45	3.4e-28
	END AA	346	272	344	347	183	371
	START AA	281	109	193	861	27	285
	CHAIN	A	¥ ,	A	A	A	A
	PDB ID	1trc	1vrk	lvrk	lvrk	1 vrk	lvrk
;	NO E	1156	1156	1156	1156	1156	1156

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	PDB annotation		STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY. GMPPNP, GPPNHP.	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2- ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR- LIKE REPEAT, PROTEIN TRANSPORT
	Compound	CALCTUM-BINDING PROTEIN SARCOPLASMIC CALCTUM- BINDING PROTEIN (ISO TYPE II) 2SAS 3	ALPHA SPECTRIN; CHAIN: A, B, C;	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, I, L, N, P;	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;
Table 5	SEQ FOLD	50.84				
Tal	PMF score		0.07	0.05	0.04	0.00
	Verify score		-0.15	-0.58	-0.25	-0.17
	Psi Blast	8e-20	4.8e-10	0.0072	9600.0	7.2e-14
	END	288	286	355	308	244
!	START AA	. 68	08	222	132	19
	CHAIN		∀	A	⋖	А
	PDB ID	2sas	1cum	1f5n	1fqv	1qqe
	SEQ D	NO:	1157	1157	1157	1157

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	PDB annotation	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE	TYROSINE PHOSPHATASE SYP, SHPTP-2; TYROSINE PHOSPHATASE, INSULIN SIGNALING, SH2 PROTEIN		CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN	CALCIUM-BINDING
	Compound	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	PYST1; CHAIN: NULL;	SHP-2; CHAIN: A, B;	:	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA);
Table 5	SEQ FOLD score								
Tal	PMF	0.13	0.33	0.45	0.01		0.57	0.04	-0.05
ļ	Verify score	-0.16	-0.10	90.0	-0.16		0.76	0.15	0.13
	Psi Blast	3.6e-23	3.4e-20	1.4e-16	3.4e-57		1.7e-28	7.2e-11	5.1e-26
	END	355	256	206	207			470	476
	START AA	97	28	59	8		222	367	389
	CHAIN ID	A	A		Ą		A	A	A
	PDB ID	1quu	1d5r	1mkp	2shp		1a25	1a25	1a25
	SEQ ID NO:	1157	1159	1159	1159			1165	1165

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	PDB annotation	PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSI S SYNAPTOTAGMIN, C2- DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSI S	ENDOCYTOSIS/EXOCYTOSI S SYNAPTOTAGMIN, C2- DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSI	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID- BINDING, HYDROLASE	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID- BINDING, HYDROLASE	LIPID DEGRADATION PLC- D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM- BINDING, PHOSPHOLIPASE
	Compound	CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;
Table 5	SEQ FOLD score						
Та	PMF		0.75	0.16	-0.01	0.19	-0.09
	Verify score		0.64	-0.04	0.35	-0.35	0.50
	Psi Blast		3.4e-35	6.8e-16	5.1e-16	1.4e-09	3.4e-24
	END		348	473	335	466	359
	START AA		222	389	237	389	239
	CHAIN		A	A	А	A	V
44	PDB ID		lbyn	16yn	1cjy	1cjy	1djx
	SEQ D Q		1165	1165	1165	1165	1165

lable 5	SEQ Compound PDB	FOLD	score	C. 3 PHOSPH
-			score	,
	PMF	score		
	Verify	score		
	Psi	Blast		
	CINE	AA.		
	START	Ψ¥		
	CHAIN	О		

	PDB annotation	C, 3 PHOSPHOINOSITIDE- SPECIFIC	LIPID DEGRADATION PLC-	D1; PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE,	LIPID DEGRADATION, 2	TRANSDUCER, CALCIUM-	BINDING, PHOSPHOLIPASE	C, 3 PHOSPHOINOSITIDE-	LIPID DEGRADATION PLC-	DI: PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE,	LIPID DEGRADATION, 2	TRANSDUCER, CALCIUM-	BINDING, PHOSPHOLIPASE	C, 3 PHOSPHOINOSITIDE-	SPECIFIC	LIPID DEGRADATION PLC-	D1; PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE,	LIPID DEGRADATION, 2	TRANSDUCER, CALCIUM-	BINDING, PHOSPHOLIPASE	C, 3 PHOSPHOINOSITIDE-	SPECIFIC	ENDOCYTOSIS/EXOCYTOSI	S BETA SANDWICH,	CALCIUM ION, C2 DOMAIN	ENDOCYTOSIS/EXOCYTOSI S BETA SANDWICH,
	Compound		PHOSPHOINOSITIDE-SPECIFIC	PHOSPHOLIPASE C, CHAIN: A,	B;					PHOSPHOINOSITIDE-SPECIFIC	PHOSPHOLIPASE C. CHAIN: A.	B;						PHOSPHOINOSITIDE-SPECIFIC	PHOSPHOLIPASE C, CHAIN: A,	B;						SYNAPTOTAGMIN III; CHAIN: A;			SYNAPTOTAGMIN III; CHAIN: A;
able 5	SEQ FOLD score	,																								:			
Ta	PMF		0.04							-0.08								0.00								0.05			0.98
	Verify score		0.16					0.69	0.69						-0.13							0.16			0.19				
	Psi Blast		6.8e-19					3.4e-24	3.4e-24						6.8e-19						6.8e-50			5.1e-63					
	END		479							359	_							479								358			487
	START AA		389							239				-				389								122			224
	CHAIN		A	-						В			-					В								A			А
	PDB ID	PDB Idjx					1djx	1djx						1djx						ldqv			ldqv						
	SEQ No. to Si		1165		-					1165								1165								1165			1165

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	PDB annotation	CALCIUM ION, C2 DOMAIN	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING	PROTEIN, CALCIUM-	BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE,	PROTEIN KINASE C	TRANSFERASE CALCIUM++,	PROTEIN, CALCIUM-	BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE,	PROTEIN KINASE C	TRANSFERASE CALCIUM++,	PHOSPHOLIPID BINDING	PROTEIN, CALCIUM-	BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE,	PROTEIN KINASE C	HYDROLASE CALB	DOMAIN; HYDROLASE, C2	DOMAIN, CALB DOMAIN								TO COMPANY CYPICALLY MANY COMPANY COMPANY	ENDOCYTOSIS/EXOCYTOSI
	Compound		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;					PROTEIN KINASE C, ALPHA	IIIE, CHAIN. A,				PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;					PHOSPHOLIPASE A2; CHAIN:	NULL;		CALCIUM/PHOSPHOLIPID	BINDING PROTEIN	SYNAPTOTAGMIN I (FIRST C2	DOMAIN) (CALB) 1RSY 3	CALCIUM/PHOSPHOLIPID	BINDING PROTEIN	SYNAPTOTAGMIN I (FIRST C2	DOMAIN) (CALB) IRSY 3	KABPHILIN 3-A; CHAIN: A;
Table 5	SEQ FOLD score																													
Ta	PMF		0.13					0.03					0.01						-0.01			0.74				0.01			700	0.04
	Verify score		0.45					0.19					-0.09						0.11			0.57				0.17			17	0.4/
ļ	Psi Blast		6.8e-31					3.6e-11					3.4e-26						5.1e-16		,	6.8e-35				6.8e-16			30	8.56-25
	END		351					470					476						335			340				473			7.7.6	555
	START		221					367					389						237			222				389			700	477
	CHAIN		_ V					A					A																	A
	PDB ID		1dsy					1dsy					1dsy					i 	1rlw			lrsy				Irsy			-	Srpb
	Š a Š		1165					1165					1165				-		1165		,	1165				1165			11/6	C011

	PDB annotation	S C2-DOMAINS, C2B- DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSI S	ENDOCYTOSIS/EXOCYTOSI S C2-DOMAINS, C2B- DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSI S	 COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC			
	Compound		RABPHILIN 3-A; CHAIN: A;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;
Table 5	SEQ FOLD score						76.10	
Tal	PMF score		0.13	1.00	86.0	1.00		1.00
	Verify score		0.40	0.26	0.28	0.50		0.27
	Psi Blast		6.8e-29	3.4e-26	2e-26	1.7e-30	6e-44	6e-44
	END AA		488	 208	209	376	378	378
	START AA		357	135	135	296	296	296
	CHAIN		Ą	 4	<	A	A	A
	PDB ID		Згрь	laih	lalh	lalh	lalh	lalh
	SEQ ID NO:		1165	 1172	1172	1172	1172	1172

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	PDB annotation	FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA, INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
	Compound	CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score					
Tal	PMF		0.03	1.00	1.00	1.00
	Verify score		0.27	0.22	08.0	0.59
	Psi Blast		3.4e-37	1.7e-44	1.5e-48	6.8e-50
	END		180	208	236	264
	START		102	128	155	183
	CHAIN		U	၁	S	၁
	ED CI		1mey	1mey	lmey	lmey
	A A B B B B B B B B B B B B B B B B B B		1172	1172	1172	1172

	PDB annotation		(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,
	Compound			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER
Table 5	SEQ	FOLD		102.15				-																							
Tal	PMF	score							1.00							1.00							1.00							1.00	
	Verify	score							0.75							0.54							0.73							0.57	
	Psi	Blast		3.4e-50					3.4e-50				_			3.4e-50			_				8.5e-51				,	-		1.2e-50	
		AA		265					292							320							348				_			376	
	START	AA		183					211							239							267					•		295	
	CHAIN	a		ပ					С							ر د							သ							၁	
	PDB			1mey			•		lmey							lmey							lmey				_			lmey	
	SEQ	∃ Ö		1172					1172							1172							1172							1172	

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	PDB annotation	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION
	Compound	PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
Table 5	SEQ FOLD score					
Lat	PMF		0.76	0.46	86.0	0.63
	Verify score		80.0	0.07	-0.03	0.52
	Psi Blast		8.5e-49	5.1e-30	2e-57	8.5e-34
j	END		405	245	292	273
	START		323	109	131	135
	CHAIN		U	A	¥	A
	PDB ID		1mey	11f6	1466	1tf6
	SEQ NO:		1172	1172	1172	1172

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	PDB annotation		REGULATION/DNA), RNA	POLYMERASE III, 2 TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGIT ATTOMENA)
	Compound						TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D, 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE: CHAIN:
Table 5	SEQ	Score					104.46										-								•		_	*		
Та	PMF	SCOILE												1.00								1.00								0.90
	Verify	score												0.26								0.27								-0.13
	Psi Dlagt	Diast					1.4e-72							5.1e-37								1.4e-72								8e-44
	END	77					349							329								376								418
	START	AG					183							184								212								268
	CHAIN	9	-				V			-		_		A								¥								A
	PDB m	3			-		1116							1476				_			100									1#6
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	PDB annotation		COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA	TRANSCRIPTION	INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	מסיים שיים היים יים יים יים יים יים יים יים יים
!	Compound		B, C, E, F;			TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN: B C E F:						YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	INITIATOR ELEMENT DNA;	CHAIN: A, B;				
Table 5	SEQ	FOLD score																										
Tal	PMF	score				0.57							0.71								1.00							
	Verify	score				-0.24							0.21								0.19							
	Psi	Blast				6.8e-37							3.4e-29								4e-39							
	END	AA				454							208				-				236							
	START	AA				296							110								128							
	CHAIN					A							ပ								ပ							
	PDB					1466							lubd								lubd 1							
	SEQ	H Ö				1172							1172								1172							

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	PDB annotation		REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION
	Compound			YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATIOR ELEMENT DNA;	CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;
Table 5	SEQ FOLD	score							-																					
Ta	PMF score			1.00						1.00									1.00									1.00		
	Verify score			0.47						0.50									0.43									0.18		
	Psi Blast			8.5e-33						1.4e-34									1.6e-52									5.1e-34		
:	END AA			236						264				-					292	-								320		
	START			135					-	163							•		182					-				219		
	CHAIN			ن ن						၁									ပ									၁		
	PDB ID			lubd			_			1ubd	*			_					lubd						-			1nbd	-	
	SEQ D	NO:		1172						1172									1172			•						1172		

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	PDB annotation	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONDNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATON INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3
	Compound	CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD score		84.85	-	
Tal	PMF			1.00	0.88
	Verify score			0.02	0.04
	Psi Blast		6e-54	6e-54	1.8e-38
	END		349	376	390
	START		241	265	293
	CHAIN		ပ	O	ပ
	PDB		1ubd	lubd	lubd
	S D S		1172	1172	1172

	1														_									_						_
	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION PEGIII ATTON/DMA) VENIC	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (DNA-BINDING	FROI EIN/DNA) FIVE-
	Compound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRIS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						ZINC FINGER PROTEIN GLII;	CHAIN, A, DINA; CHAIN: C, D;
Table 5	SEQ FOLD score																													
Ta	PMF		0.16								0.10								,	-0.15									0.78	
	Verify		-0.00								-0.43								000	0.08									0.39	
	Psi Blast		1.7e-32								1.5e-29									16-21									1./e-32	
E	AA		406							007	458	•							100	180									735	
T. C. 4 T.C.	SIAKI	000	303				-			171	331								00	06									/01	
CITATA	CHAIN		ပ								ر								ر)		•							¥	
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CEO	ğ a ö	27.7	7/11							1173	7/11								1172	7/17								117	7/11	

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	PDB annotation	FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	FROTELINIDINA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- RINDING PROTENVINA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC FINGER COMPLEX (DNA.	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC
	Compound		ZINC FINGER PROTEIN GLII; CHAIN: A: DNA: CHAIN: C D:	CIRLLY, CIRLLY, C. D.	ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GL11;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;	
Table 5	SEQ FOLD score						-		93.54	_					•	-				•	•					
Ta	PMF		86.0		1.00									1.00					1.00					0.36		
	Verify score		09.0		0.27									0.49					0.05					-0.08		
	Psi Blast		3.4e-34		8e-52	-			2e-69					2e-67			-		2e-69					1e-32		
	END		263		266				294					350					376					406		
	START		128		135				157					183					211					275		
	CHAIN		A		Ą				A					A					¥					Ą		
	PDB		2gli		2gli				2gli	,				2gli					2gli					2gli		
	SEQ ID NO:		1172		1172				1172					117.2		_		\dashv	1172					1172		

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	uo		(DNA- DNA)		PLEX), ZINC	ING		PLEX), ZINC	ING			PLEX), ZINC	ING	-		PLEX), ZINC	ING		gaoina	ringen,		TEIN		LEX		
	PDB annotation		FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (ZINC	FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC	FINGER/DNA) COMPLEX	(ZINC FINGEK/DNA), ZINC	FINGER, DNA-BINDING	PKOIEIN	COMPLEX (ZINC	FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC	FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER	PROFINITION PAIN	FRO I EIIN-DINA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAI	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC
	Compound			OGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGOINOCLEO I IDE BINDING	SITE; CHAIN: B, C;		QGSK ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;		QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;		DNA; CHAIN: A, B, D, E;	DROTEIN: CHAIN: OF G.	INCIPLIA, CIPLIA, C, I', C,					DNA; CHAIN: A, B, D, E;
Table 5	SEQ	score		52.45									-	-			_												63.59
Ta	PMF	SCOLE					0.94				,	7.08 1.08					1.00					0.05							
	Verify	score					0.37					0.50					0.57					0.11							
	Psi Blact	Diast		1.4e-27			6.8e-26				,	1./e-25		-			1.4e-27			-		6.8e-44							6.8e-44
	END	4		70	_		98				0	2					70			-		125				_			96
	START	4		-			16					4					5					15							15
	CHAIN	3		¥			Ą					¥					¥					ပ							C
	10B	3		lalh			lalh				11.	1210					lalh					lmey							Imey
	SE E	g ö		1174	-		1174				1177	11/4					1174				-	117/4						┰	1174

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	PDB annotation		FINGER/DNA) ZINC FINGER,	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DINA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-
	Compound		CONSENSUS ZINC FINGER PROTEIN: CHAIN: C. F. G.				DNA. CHAMI. A D D.	CONSENSITE AND ENICED	PROTEIN; CHAIN; C. F. G.					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5
Table 5	SEC.	rolld																													
Ta	FIMIF	score					9	7.00						-0.05							-0.19			_						0.21	
J. 11	verny	score					0.39							0.08							0.05									-0.08	
	Place	Diast					6.8e-39						,	5.le-13						1	2.1e-7/					-				1./e-2/	
CING		۲ ۷					89	•				_	000	607							740									c71	
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	PDB annotation	YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	TRANSCRIPTION TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER NAR	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	COMPLEX (TRANSCRIPTION
	Compound	INITIATOR ELEMENT DNA; CHAIN: A, B;	ADR1; CHAIN: NULL;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S
Table 5	SEQ FOLD score		54.11					
Ta	PMF			0.16		0.09	0.07	0.24
	Verify score			-0.13		-0.53	-0.65	-0.57
	Psi Blast		1.5e-17	6.8e-27		0.00018	0.0014	0.00014
	END AA		76	127		158	158	158
	START AA		16	5		107	107	107
	CHAIN			A		∢	O	A
	PDB TD		2adr	2gli	,	lalh	lmey	1tf6
0	H H H		1174	1174	7.0	1176	1176	1176

	PDB ar			REGULATION
	Compound			RIBOSOMAL RNA GENE: CHAIN: REGULATION
Table 5	SEQ	FOLD	score	
Ta	PMF	score		
	Verify	score	!	
	Psi	Blast		
	END	AA		
	START	AA		-
	CHAIN			

	PDB annotation	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR			SIGNALING PROTEIN 11 ALPHA-HELICES	PHOSPHOTRANSFERASE C- SRC, P60-SRC; SRC,	TYROSINE KINASE, PHOSPHORYLATION. SH2.	SH3, 2 PHOSPHOTYROSINE,	PROTO-ONCOGENE, PHOSPHOTRANSFERASE	TRANSFERASE PROTO- ONCOGENE TYROSINE	KINASE; PROTO-	ONCOGENE, TRANSFERASE,	KINASE, 2
	Compound	RIBOSOMAL RNA GENE; CHAIN: RIB, C, E, F; CC RIB	ADRI; CHAIN: NULL; RI TI TI RI RI RI RI		PHOSPHOTRANSFERASE C-SRC KINASE (SH3 DOMAIN) (E.C.2.7.1.112) 1CSK 3		TYROSINE-PROTEIN KINASE PI SRC; CHAIN: NULL;	T	IS	II II	PHOSPHOTRANSFERASE FYN; TI CHAIN: A: 3BP-2: CHAIN: B: O		0 -	X K
Table 5	SEQ FOLD score					!								
Tak	PMF		0.03	,	0.76	0.80	0.12				0.59			
	Verify score		-0.31		0.28	0.11	0.16				0.50			
	Psi Blast		0.0004		4.8e-13	2.4e-33	6.8e-19				2.4e-14			
	END AA		159		572	340	596				573			
	START AA		107		518	172	517				513			
	CHAIN				¥	A					A			
ļ	PDB ID		2adr	1	lcsk	1f5x	1fmk				1fyn			
i	SEQ NO.		1176	\dashv	1180	1180	1180				1180			

	PDB annotation	PHOSPHORYLATION, ATP- BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PE PTIDE)	TRANSFERASE PROTO- ONCOGENE TYROSINE KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP- BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PE PTIDE)		COMPLEX (KINASE/PEPTIDE)	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN,
	Compound		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	P56—LCK— TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15	ALPHA SPECTRIN; CHAIN: NULL;
Table 5	SEQ FOLD score					
Tal	PMF		0.78	69.0	0.01	0.87
	Verify score		0.18	0.29	00.0-	0.35
	Psi Blast		1.46-12	1.2e-12	3.4e-13	1.2e-12
;	END AA		574	573	598	573
	START		514	517	524	513
	CHAIN		¥		A	
	PDB ID		1fyn	1gfc	Ilck	lpwt
	SEQ ID NO:		1180	1180	1180	1180

	PDB annotation	CVTOSKEI ETON	TYROSINE KINASE TYROSINE KINASE- INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED	ACTIVATION LOOP	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE		INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHII IC A DHESTON	CELL ADHESION NEURAL	CELL ADHESION NEURAL	CELL ADHESION NEURAL
	Compound		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3	HEMATOPOIETIC CELL KINASE; CHAIN: NULL;		HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;
Table 5	SEQ FOLD	21000					105.23					
Ta	PMF		0.07	0.76	0.63			0.04	0.10	90.0	0.52	0.30
	Verify score		-0.18	0.34	-0.11		,	-0.34	-0.28	0.20	-0.11	-0.20
	Psi Blast		3.4e-16	1.7e-12	1.1e-12		5.1e-35	1.7e-46	5.1e-32	1.7e-25	1.4e-35	3.4e-36
	END AA		865	574	575		1819	1951	586	1621	595	979
	START AA		513	517	518		1428	1536	252	1413	211	290
	CHAIN		∀	A			A	A	∢	А	A	A
	PDB ED		1qcf	lshf	4hck	:	loih	lbih	1bih	1cs6	lcs6	1cs6
			1180	1180	1180	1105	1183	1185	1185	1185	1185	1185

	PDB annotation	CELL ADHESION	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN- LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH	FACTON GROWIN FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF,	FGFR, IMMUNOGLOBULIN- LIKE, SIGNAL	TRANSDUCTION, 2	DIMERIZATION, GROWTH	RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF,	FGFK, IMMUNOGLOBULIN- TIKE SIGNAT	TRANSDUCTION, 2	DIMERIZATION, GROWTH	FACTOR/GROWTH FACTOR	RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF,	FGFR, IMMUNOGLOBULIN-	LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION, GROWTH
	Compound		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST	GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;				FIBROBLAST GROWTH FACTOR	CROWITH EACTOR DECERTOR 1.	CHAIN: C. D:					FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B; FIBROBLAST	GROWTH FACTOR RECEPTOR 1;	CHAIN: C, D;	
Table 5	SEQ FOLD score																				
Ta	PMF		-0.05		0.52					0.36							0.03				
	Verify score		0.14		-0.30					-0.01							0.10				
	Psi Blast		3.4e-26		5.1e-21					4e-15	_					100	3.4e-25				
	END AA		1620		381					409						000,	0701				
	START AA		1439		255					291						1420	1439				
	CHAIN		Ú		ပ					ပ					-	-	۵				
	E E		Icvs		Icvs					lcvs						10.0	ICVS				
	N H N O N	,	S8 1		1185					1185						1105					

	PDB annotation	FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF.	FGFR, IMMUNOGLOBULIN- LIKE, SIGNAI	TRANSDUCTION, 2	DIMERIZATION, GROWTH	FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF,	FGFR, IMMUNOGLOBULIN-	LIKE, SIGNAL	TRANSDUCTION, 2	DIMERIZATION, GROWTH	FACTOR/GROWTH FACTOR	KECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF,	FGFR, IMMUNOGLOBULIN-	LIKE, SIGNAL	IKANSDUCTION, 2	DIMERIZATION, GROWTH	FACTOR/GROWTH FACTOR	RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF,	FGFR, IMMUNOGLOBULIN-	LIKE, SIGNAL	TRANSDUCTION, 2
	Compound		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST	GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	`			FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B; FIBROBLAST	CHAIN: C D.	CITALY: C, D,				TITLE CHE LANGE CONTRACTOR	FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B; FIBROBLAST	GROW I H FACTOR RECEPTOR 1;	CILMIN. C, D;					FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B; FIBROBLAST	GROWTH FACTOR RECEPTOR 1;	CHAIN: C, D;	
Table 5	SEQ FOLD	SCOTE														•										-		
Ta	PMF		0.07					0.24							0,70	0.40						-	5	05.0		-		1
	Verify score		-0.17					-0.29							0.05	0.00							200	07.0				
	Psi Blast		1.5e-42					8.5e-21							21011	5.46-14							1 10 17	1.46-1/				
	END		1951					381							602	700							613	710				
	START AA		1728				}	255							503	COC						,	505	3				
	CHAIN		О					<u> </u>	_						- -	٦								-				
	PDB ID		lcvs					Icvs		_	-				lcvs	2							1 rve	2				
	SEQ B B SS		1185			-	100	C811					_		1185								1185	2				
										_			_					_		_	_							

PDB CHAIN START END																															
PDB		PDB annotation	DIMERIZATION, GROWTH	FACTOR/GROWTH FACTOR RECEPTOR	CELL ADHESTON NCAM:	NCAM, IMMUNOGLOBULIN	FOLD, GLYCOPROTEIN	CELL ADHESION NCAM; NCAM, IMMI INOG! OBIT! IN	FOLD, GLYCOPROTEIN	CELL ADHESION NCAM;	NCAM, IMMUNOGLOBULIN	FOLD, GLYCOPROTEIN	CELL ADHESION NCAM;	NCAM, IMMUNOGLOBULIN	FOLD, GLYCOPROTEIN	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2;	FGFR2; IMMUNOGLOBULIN	(IG)LIKE DOMAINS	BELONGING TO THE I-SET 2	SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2;	FGFR2; IMMUNOGLOBULIN	(IG)LIKE DOMAINS	BELONGING TO THE I-SET 2	SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2:
PDB		Compound			NEURAL CELL ADHESION	MOLECULE; CHAIN: A, B, C, D;	NIETID AT CITET ATTENDED	NEUKAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;		NEURAL CELL ADHESION	MULECULE; CHAIN: A, B, C, D;	MEI TO AT CHIT A PETER CO	MOI FOUR E. CELL ADHESION	MOLLEY CALMIN: A, B, C, U;	TIPP OF 1 OF CE CE	FIBROBLAST GROWTH FACTOR	ETH OF AGE OF COMMEN	FIBROBLAST GROWTH FACTOR	KECEPIOK 2; CHAIN: E, F, G, H;				FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B, C, D;	FIBRUBLASI GROWTH FACTOR	RECEPTOR 2; CHAIN: E, F, G, H;				FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B, C, D;
PDB CHAIN START END Psi Verify PM	ble 5	SEQ FOLD	21026																,						-						
PDB CHAIN START END Psi	Ta	PMF			0.15		77.0	77.0	(0.00		0.18	0.10		000	50.0-						5	0.01			-			3	0.40	1
PDB CHAIN START END	17	Verify score			0.11	_	0.15	3.	4	0.10		0.44	-		0.15	3.0						0.01	-0.01						4	0.19	
PDB CHAIN START DD DD AA AA AA AA AA A	Do:	FS1 Blast			3.4e-20		4e-27	î D	1 70 22	1./5-22		1e-15)		3 4e-21	3						10.15	C1-24						20 16	01-27	
PDB CHAIN D D D D D D D D D	FNT	AA			1622		1952		171			597			1620) 					···	1634	1001	_				· · · · · ·	305		
PDB ID Iepf Iepf A Iepf A Iev2 E	START	AA		1 407	1485		1730		308	0		504			1443							1527							201		
PDB ID	CHAIN	A D			₩		A		A	4		A			E						_	П							[II.		
	PDB	<u>a</u>		1000	זלטו		1epf		1enf	<u>.</u>		lepf			lev2														1ev2		
SEQ DD NO: 1185 1185 1185 1185	SEO	N B B		1185	611		1185		1185			1185			1185							1185							1185		

	PDB annotation		FGFR2; IMMUNOGLOBULIN	BELONGING TO THE I-SET 2.	SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2;	FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS	BELONGING TO THE I-SET 2	SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2;	FGFR2; IMMUNOGLOBULIN	(IG)LIKE DOMAINS	BELONGING TO THE I-SET 2	SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2;	FGFR2; IMMUNOGLOBULIN	(IG)LIKE DOMAINS	BELONGING TO THE I-SET 2	SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF1;	FGFR1; IMMUNOGLOBULIN	(IG) LIKE DOMAINS	BELONGING TO THE I-SET 2
	Compound		FIBROBLAST GROWTH FACTOR RECEPTOR 2- CHAIN: F F G H:				FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E. F. G. H:				FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR	RECEPTOR 2; CHAIN: E, F, G, H;				FIBROBLAST GROWTH FACTOR	2; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR	RECEPTOR 2; CHAIN: E, F, G, H;				FIBROBLAST GROWTH FACTOR	1; CHAIN: A, B; FIBROBLAST	GROWTH FACTOR RECEPTOR 1;	CHAIN: C, D;	
Table 5	SEQ	FOLD																													
Ta	PMF	score					0.39						0.16						;	0.23							90.0-				
	Verify	score					0.19						-0.16						,	-0.46							0.24				
	Psi	Blast					1.7e-24						8.5e-41							6.8e-20							3.4e-24				
		AA					1624						1951							285							1620				
	START	AA				,	1443						1728	-					000	557							1439				
	CHAIN	∍					5						5					_		5							ပ				
	PDB	a				,	lev2					,	lev2						,	lev2							levt				
	SEQ	NÖ E				,	5811					,	1185						1105	1185							1185				

			T				T					Γ_			Γ.		_	_		_							
	PDB annotation	SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1;	FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS	BELONGING TO THE L-SET 2	SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	IMMUNE SYSTEM FC-	EPSILON RI-ALPHA;	IMMUNOGLOBULIN FOLD,	GLICOFROIEIN,	PROTEIN	CONTRACTILE PROTEIN	IMMUNOGLOBULIN FOLD,	BETA BARREL	CONTRACTILE PROTEIN	IMMUNOGLOBULIN FOLD,	BEIA BARREL	CONTRACTILE PROTEIN	IMMUNOGLOBULIN FOLD,	BETA BARREL	CONTRACTILE PROTEIN	IMMUNOGLOBULIN FOLD,	BETA BARREL	CONTRACTILE PROTEIN	IMMUNOGLOBULIN FOLD,	BETA BARREL	CONTRACTILE PROTEIN
	Compound		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST	GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;			HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A;			TELOKIN; CHAIN: A			TELOKIN; CHAIN: A			TELOKIN; CHAIN: A			TELOKIN; CHAIN: A			TELOKIN; CHAIN: A		THE THE THE	IELOKIN; CHAIN: A
Table 5	SEQ FOLD																										
Ta	PMF		0.11				-0.05					08.0			1.00			0.87		,	1.00	-		0.55		50	1.00
	Verify score		-0.29				0.15					0.58		ļ	0.04			0.41			0.60			0.15		300	0.33
	Psi Blast		1.2e-19				80-99					5.1e-20			3.4e-24			6.8e-24			1.7e-22			1e-20		40.01	17-24
	END		381				386					1620			1819			1951		000	382			591		200	299
	START		255				291					1528			1721			1854		, 00	784			498		502	coc
	CHAIN		ت ن				Α					A			₩			W W	•		A			A		<	4
	PDB ID		levt				1£2q			_		1fhg			lfhg		,	lthg		5	Ting			lfhg		1434	TIME
	S		1185				1185					1185			1185		0,7	C811		1106	1185			1185		1185	1100

	PDB annotation	IMMUNOGLOBULIN FOLD, BETA BARREL			COMPLEX (IMMUNOGLOBULIN/RECEP TOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,	GLI COFRO LEIN, RECEPTOR, 2 SIGNAL, COMPLEX (TAMATINOGI ORI II IN/BECED	TOR)	COMPLEX (IMMUNOGLOBULIN/RECEP TOR) IMMUNOGLOBULIN	FOLD, TRANSMEMBRANE, GLYCOPROTEIN,	RECEPTOR, 2 SIGNAL, COMPLEX	(IMMUNOGLOBULIN/RECEP TOR)	COMPLEX	(IMMUNOGLOBULIN/RECEP TOR) IMMUNOGLOBULIN	FOLD, TRANSMEMBRANE, GLYCOPROTEIN,
!	Compound		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;			INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;				INTERLEUKIN-1 BETA; CHAIN:	A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	
Table 5	SEQ FOLD score													
Ta	PMF		-0.14	-0.15	0.00			0.09				0.03		
	Verify score		0.12	0.10	-0.28			-0.53				-0.42		
	Psi Blast		6e-10	2e-14	1e-21			1.2e-22				5.1e-18		
	END AA		386	596	1950			009				290		
	START AA		297	509	1719			305				322		
	CHAIN		А	A	Д			Ф			,	В		
	PDB ID		lhng	1hng	litb			lifb				lifb		
	SEQ NO:		1185	1185	1185			1185				1185		

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	PDB annotation		RECEPTOR, 2 SIGNAL,	(IMMUNOGLOBULIN/RECEP	TOR)	KINASE KINASE, TWITCHIN, INTRASTERIC REGIT ATTON	KINASE KINASE, TWITCHIN,	KINASE KINASE, TWITCHIN	INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN,	INTRASTERIC REGULATION	KINASE KINASE, I'WII'CHIN, INTRASTERIC REGIII ATION								MUSCLE PROTEIN	CONNECTIN, NEXTM5; CELL	ADHESION,	GLYCOPROTEIN,	TRANSMEMBRANE,	REPEAT, BRAIN, 2	IMMUNOGLOBULIN FOLD,	ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE
,	Compound					TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: NULL;		TWITCHIN; CHAIN: NULL;	TWITTCHIN. CHAIN: NHH I.	I WILCILLY, CAIALLY: INOLL;	IMMUNOGLOBULIN	IMMINOGI OBLIL IN G1 (1991)	(MCG) WITH A HINGE	DELETION 1MCO 3	IMMUNOGLOBULIN	IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE	DELETION 1MCO 3	TITIN; CHAIN: NULL;							
Table 5	SEQ FOLD	score											110.47	•													
Ta	PMF					0.59	0.52	06.0		06.0	0.77	 			•		0.04			0.55							
	Verify score					0.59	0.37	0.97		0.44	95 0						-0.48			0.35							
	Psi Blast				,	1.2e-15	3.4e-17	3.4e-18		6.8e-15	8.5e-16		3.4e-12				3.4e-12			4e-20							
	END AA				1,000	1620	1818	1952		387	590	;	1927				1934		,	1620							
	START				1522	1333	1725	1859	000	293	500		1524				1542			1550							
	CHAIN												Н			,	H						_				
1	PDB ID				11,00	IKOZ	lkoa	1koa	11.	IKOa	1koa		1mco		-	,	ımco			ıncı							
040) E E E				1185	1100	1185	1185	1105	1183	1185		1185			0,1	1185		1105	1100							

	PDB annotation	PROTEIN	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION,	GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2	IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING,	SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN CONNECTIN, NEXTMS; CELL	ADHESION,	GLYCOPROTEIN, TRANSMEMBRANE	REPEAT, BRAIN, 2	IMMUNOGLOBULIN FOLD, AI TERNATIVE SPITCING	SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN	CONNECTIN, NEXTM5; CELL	ADHESION, GLYCOPROTFIN	TRANSMEMBRANE,	REPEAT, BRAIN, 2	IMMUNOGLOBULIN FOLD,	ALTERNATIVE SPLICING,	SIGNAL, 3 MUSCLE PROTEIN
	Compound		TITIN; CHAIN: NULL;				TITIN; CHAIN: NULL;						TITIN; CHAIN: NULL;							
Table 5	SEQ FOLD score																			
Ta	PMF		0.28				0.40						0.16							
	Verify score		0.53				-0.10						0.21							
	Psi Blast		3.4e-16				2e-20						5.1e-19				-			
	END		1621		·		1817						1819							
	START AA		1533				1722	-					1729							
	CHAIN									-5,1				=						
	PDB		Inct				ınct						Inct							
	N E S		5811			1	2811	_					1185							

	PDB annotation	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MISCLE	PROTEIN MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN
	Compound	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;
Table 5	SEQ FOLD score				
Ta	PMF	0.51	0.25	1.00	0.99
	Verify score	0.20	0.51	0.54	0.41
	Psi Blast	6e-22	5.1e-18	1.2e-19	1e-18
	END AA	1950	1951	382	382
	START	1858	1863	291	293
	CHAIN				
	PDB ID	lnct	lnct	lnct	1nct
	SEQ NO:	1185	1185	1185	1185

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	PDB annotation	CONNECTIN, NEXTMS; CELL ADHESION,	TRANSMEMBRANE,	REPEAT, BRAIN, 2 IMMINOGLOBITIN FOLD	ALTERNATIVE SPLICING,	SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN	CONNECTIN, NEXTIMS; CELL	ADHESION, GI VCOPROTHIN	TP ANSWENDER AND	REPEAT. BRAIN. 2	IMMUNOGLOBULIN FOLD,	ALTERNATIVE SPLICING,	SIGNAL, 3 MUSCLE	PROTEIN	MUSCLE PROTEIN	ADHESION,	GLYCOPROTEIN,	TRANSMEMBRANE,	REPEAT, BRAIN, 2	IMMUNOGLOBULIN FOLD,	ALTERNATIVE SPLICING,	SIGNAL, 3 MUSCLE	PROTEIN	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN 127,
	Compound						TITIN; CHAIN: NULL;									TITIN; CHAIN: NULL;									TITIN, 127; CHAIN: NULL;
rable 5	SEQ FOLD score													-											
Та	PMF						0.99									0.99									0.65
	Verify						0.02									0.51									0.64
	Psi Blast						4e-22									3.4e-18									6e-17
	END				-		597									595						-			1614
	START AA						503	_								509									1531
	CHAIN			-												-							-		
	PDB						lnct									Inct							•		ltit
	SEQ NO:						1185									1185									1185

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	PDB annotation		TITIN IG REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE	DOMAIN	IMMUNOGLOBULIN-LIKE	DOMAIN CONNECTIN 127, TITIN IG REPEAT 27:	MUSCLE PROTEIN,	IMMUNOGLOBULIN-LIKE DOMAIN	IMMUNOGLOBULIN-LIKE	DOMAIN CONNECTIN 127,	TITIN IG REPEAT 27;	MUSCLE PROTEIN,	IMMUNOGLOBULIN-LIKE	DOMAIN	IMMUNOGLOBULIN-LIKE	DOMAIN CONNECTIN 127,	TITIN IG REPEAT 27;	MUSCLE PROTEIN,	IMMUNOGLOBULIN-LIKE DOMAIN									
	Compound				TITIN, 127; CHAIN: NULL;				TITIN, 127; CHAIN: NULL;						TITIN, 127; CHAIN: NULL;					MUSCLE PROTEIN TITIN	MODULE M5 (CONNECTIN)	1TNM 3 (NMR, MINIMIZED	AVERAGE STRUCTURE) 1TNM 4	1TNM 58	MUSCLE PROTEIN TITIN	MODULE M5 (CONNECTIN)	ITNM 3 (NMR, MINIMIZED	AVERAGE STRUCTURE) 1TNM 4
Table 5	SEQ	FOLD								_												٠						
Ta	PMF	score			0.21			,	0.03						0.03					0.75					0.52			
	Verify	score			0.20				0.64						0.13					0.53					0.57			
	Psi	Blast			1.2e-17				8e-19						1.2e-18					1.8e-18					3.4e-16			
		AA			1810				1949				_		594					1620					1621			
	START	AA			1728				1862						909					1533					1533			
	CHAIN	a																										
	PDB	a			1tit				1tit	-]tit					1tmm					1tmm			
	SEQ	∃ÿ			1185				1185						1185					1185					1185			

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Table 5	PDB annotation																									MUSCLE PROTEIN	IMMUNOGLOBULIN	SUPERFAMILY, I SET,	MUSCLE PROTEIN	MUSCLE FROIEIN
	Compound		1TNM 58	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN)	1TNM 3 (NMR, MINIMIZED	AVERAGE STRUCTURE) 1TNM 4	MUSCLE PROTEIN TITIN	MODULE M5 (CONNECTIN)	1TNM 3 (NMR, MINIMIZED	AVERAGE STRUCTURE) 1TNM 4 1TNM 58	MISCIE DEOTEIN TITIN	MODULE M5 (CONNECTIN)	1TNM 3 (NMR, MINIMIZED	AVERAGE STRUCTURE) 1TNM 4	1TNM 58	MUSCLE PROTEIN TITIN	MODULE M5 (CONNECTIN)	1TNM 3 (NMR, MINIMIZED	AVERAGE STRUCTURE) 1TNM 4	1TNM 58	MUSCLE PROTEIN TITIN	MODULE M5 (CONNECTIN)	1 TNM 3 (NMR, MINIMIZED	AVERAGE STRUCTURE) 1TNM 4	1TNM 58	TWITCHIN 18TH IGSF MODULE;	CHAIN: NULL;		TWITCHIN 18TH IGSE MODIII E:	I WII CRIM TOTH MODE MICHOLE,
	SEQ	FOLD						•																						
	PMF	score		0.34			0.82				0.03	2				1.00					1.00					0.04			00.0	-0.0%
	Verify	score		0.40			0.62				0.40	2				0.53					60.0					0.18			0.55	0.0
	Psi	Blast		5.1e-19			1e-20				10-18	01-01				3.4e-18					4e-21					6e-21			10.77	77-24
	END	AA		1819			1950				387	700				595			,		297					1620			1050	1200
	START	AA		1729			1863				203	007				509					513					1529			1861	1001
	CHAIN	А																										,		
	PDB	 A		1tmm			1tmm				14mm					1tnm		•			Itmm					lwit		- * -	1 unit	Iwit
	SEQ	e ö		1185			1185				1185	6017				1185					1185					1185			1185	1100

Table 5	PDB annotation		IMMUNOGLOBULIN	SUPERFAMILY, I SET, MUSCLE PROTEIN	MUSCLE PROTEIN	IMMUNOGLOBULIN	SUPERFAMILY, I SET, MUSCLE PROTEIN	MUSCLE PROTEIN	IMMUNOGLOBULIN	SUPERFAMILY, I SET, MISCI E PROTEIN	TD ANGEED AGE TRY	RECEPTOR, RECEPTOR	TYROSINE KINASE, 3D-	DOMAIN SWAPPING, 2	TRANSFERASE	TRANSFERASE TRK	RECEPTOR, RECEPTOR	TYROSINE KINASE, 3D-	DOMAIN SWAPPING, 2	TRANSFERASE	TRANSFERASE TRK	RECEPTOR, RECEPTOR	TYROSINE KINASE, 3D-	DOMAIN SWAPPING, 2	TRANSFERASE	TRANSFERASE TRK	RECEPTOR, RECEPTOR	TYROSINE KINASE, 3D-	DOMAIN SWAPPING, 2	TRANSFERASE
	Compound		CHAIN: NULL;		TWITCHIN 18TH IGSF MODULE;	CHAIN: NULL;		TWITCHIN 18TH IGSF MODULE;	CHAIN: NULL;		RRAIN DERIVED	NEUROTROPHIC FACTOR	RECEPTOR TRKB; CHAIN: X;			BRAIN DERIVED	NEUROTROPHIC FACTOR	RECEPTOR TRKB; CHAIN: X;			NT-3 GROWTH FACTOR	RECEPTOR TRKC; CHAIN: A;				NT-3 GROWTH FACTOR	RECEPTOR TRKC; CHAIN: A;			
	SEQ	FOLD																												
	PMF	score			0.31			0.49			-0.03	3				-0.09					-0.14					0.54				
	Verify	score			0:30			0.17			98 0					0.12					0.01					0.09				
	Psi	Blast			8e-20			6e-22			le-11	· · · · · · · · · · · · · · · · · · ·				2e-11					4e-20					2e-17				
	END:	AA			381			597			1621					388					1950					597		•		
	START	AA			291			505			1554					291		-			1858					503			_	
	CHAIN					•		-			×	l				×					A					A				
	PDB	3			lwit			1wit			1wwb				,	lwwb					Iwwc					1wwc	_			
	SEQ	∃ Ä			1185			1185			1185					1185			-		1185	-				1185				

	PDB annotation		NERVE GROWTH	FACTOR/TRKA COMPLEX	BETA-NGF; COMPLEX,	TRKA RECEPTOR, NERVE	GROWTH FACTOR,	CYSTEINE KNOT, 2	IMMUNOGLOBULIN LIKE	DOMAIN, NERVE GROWTH	FACTOR/TRKA COMPLEX	NERVE GROWTH	FACTOR/TRKA COMPLEX	BETA-NGF; COMPLEX,	TRKA RECEPTOR, NERVE	GROWTH FACTOR,	CYSTEINE KNOT, 2	IMMUNOGLOBULIN LIKE	DOMAIN, NERVE GROWTH	FACTOR/TRKA COMPLEX	CELL ADHESION ICAM-2;	IMMUNOGLOBULIN FOLD,	CELL ADHESION,	GLYCOPROTEIN, 2	TRANSMEMBRANE,	REPEAT, SIGNAL	CELL ADHESION NCAM	DOMAIN 1; CELL	ADHESION,	GLYCOPROTEIN, HEPARIN-	BINDING, GPI-ANCHOR, 2	NEURAL ADHESION	MOLECULE,
	Compound		NERVE GROWTH FACTOR;	CHAIN: V, W; TRKA RECEPTOR;	CHAIN: X, Y;							NERVE GROWTH FACTOR;	CHAIN: V, W; TRKA RECEPTOR;	CHAIN: X, Y;							INTERCELLULAR ADHESION	MOLECULE-2; CHAIN: NULL;					NEURAL CELL ADHESION	MOLECULE; CHAIN: NULL;			•		
Table 5	SEQ	score																									-						
Ta	PMF	score	0.04									0.00									0.00						-0.14						
	Verify	SCOIC	0.11	_								0.16									-0.21						0.00						
	Psi Place	Diast	1.4e-14									le-16		_							6e-12						8e-16						
	END	W.	1621									597								,	1612				-		1614				-		
	START A A	VV	1534									511	-								1471				-		1530						
	CHAIN	a	×					_			,	~ ~	-			·,												_					
	PDB	3	1www							-	\dashv	MMMT									Izxd				•		Zucm						
	SEQ E	NO.	1185								0,	1185				****				,	1185					\dashv	C811				-		

														_										
	PDB annotation	IMMUNOGLOBULIN FOLD, SIGNAL	CELL ADHESION NCAM DOMAIN 1: CELL	ADHESION,	GLYCOPROTEIN, HEPARIN-	BINDING, GPI-ANCHOR, 2 NETRAL ADHESION	MOLECULE,	IMMUNOGLOBULIN FOLD,	CELL ADHESION NCAM	DOMAIN 1; CELL ADHESION,	GLYCOPROTEIN, HEPARIN-	BINDING, GPI-ANCHOR, 2 NEURAL, A DHESION	MOLECULE,	IMMUNOGLOBULIN FOLD,	CELL A DEFECTON PROFERE	NCAM MODULE 2. CFLI.	ADHESION.	GLYCOPROTEIN, HEPARIN-	BINDING, GPI-ANCHOR, 2	NEURAL ADHESION	MOLECULE,	IMMUNOGLOBULIN FOLD,	HOMOPHILIC 3 BINDING,	CELL ADHESION PROTEIN
	Compound		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;						NEURAL CELL ADHESION	MOLECULE; CHAIN: NULL;					NEURAL CELL ADHESION	MOLECULE, LARGE ISOFORM:	CHAIN: A;							NEURAL CELL ADHESION
Table 5	SEQ FOLD score					_					_												-	
Ta	Score	6	0.03						0.31						0.62									0.78
Vorify	score		-0.01						0.02						0.36									90.0
Dei:	Blast	42.10	46-19						1.4e-17		_	_			5.1e-13									1.4e-17
END	AA	1040	_	_					969			_			1622		_		•					1620
START	AA	1861	1001					100	 coc						1530									1531
CHAIN	A						•											<u>-</u>						
PDB	А	2ncm							7IICIII 7						3ncm A				···					3ncm A
SEQ	́ Q Ö	1185						1105						\rightarrow	1185 3									1185 3

	PDB annotation	NCAM MODULE 2; CELL ADHESION.	GLYCOPROTEIN, HEPARIN-BINDING GPI-ANCHOR?	NEURAL ADHESION MOI ECTITE	IMMUNOGLOBULIN FOLD.	HOMOPHILIC 3 BINDING,	CELL ADHESION PROTEIN	NCAM MODULE 2; CELL	ADHESION,	GLYCOPROTEIN, HEPARIN-	BINDING, GPI-ANCHOR, 2	NEURAL ADHESION	MOLECULE,	IMMUNOGLOBULIN FOLD,	HOMOPHILIC 3 BINDING,	CELL ADHESION PROTEIN	CELL ADHESION PROTEIN	NCAM MODULE 2; CELL	ADHESION,	GLYCOPROTEIN, HEPARIN-	BINDING, GPI-ANCHOR, 2	NEURAL ADHESION	MOLECULE,	IMMUNOGLOBULIN FOLD,	HOMOPHILIC 3 BINDING,	CELL ADHESION PROTEIN	CELL ADHESION PROTEIN NCAM MODULE 2; CELL
	Compound	MOLECULE, LARGE ISOFORM; CHAIN: A;					NEURAL CELL ADHESION	MOLECULE, LARGE ISOFORM;	CHAIN: A;								NEUKAL CELL ADHESION	MULECULE, LAKGE ISOFORM;	CIMIN. A,		-						NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM;
Table 5	SEQ FOLD score																										
Ta	PMF						0.04										0.31									;	0.64
	Verify score						-0.13									02.0	67.0										0.23
	Psi Blast						1.4e-17									1 60 20	1.05-20										8e-18
	END AA						1817							****		1052	7001										201
	START AA						1728	_						_	_	1862	7007			•			_			200	
3 7 7,500	CHAIN				_		A							-		A	•										4
444	FUB TO						3ncm									3ncm										3ncm	-
5	NO:						1185									1185										1185	

					
	PDB annotation	ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING,	CELL ADHESION FROI EIN CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING,	CELL ADHESION PROTEIN	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD PROTEIN; VISUAL ARRESTIN, DESENSITISATION OF THE VISUAL TRANSDUCTION 2 CASCADE, BINDING TO ACTICATED AND
	Compound	CHAIN: A;	NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	ARRESTIN; CHAIN: A, B, C, D;
Table 5	SEQ FOLD score				50.36
Ta	PMF		0.28	0.09	
;	Verify score		0.54	-0.25	
	Psi Blast		8e-20	1.5e-08	1.5e-48
	END AA		597	487	336
	AA		909	297	1
CHAIN			₹	A	A
pna	<u>a</u>	(oncin .	8fab	lcfl
SEO	A Ö	104	0011	1185	1197

																		\neg			_					
	PDB annotation	PHOSPHORYLATED RHODOPSIN	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD	PROTEIN; VISUAL ARRESTIN	DESENSITISATION OF THE	VISUAL TRANSDUCTION 2	ACTICATED AND	PHOSPHORYLATED	RHODOPSIN	STRUCTURAL PROTEIN	RETINAL S-ANTIGEN, 48 KD	PROTEIN; VISUAL ARRESTIN	DESENSITISATION OF THE	VISITAL TRANSDITCTION 2	CASCADE, BINDING TO	ACTICATED AND	PHOSPHORYLATED	RHODOPSIN	STRUCTURAL PROTEIN	RETINAL S-ANTIGEN, 48 KD	PROTEIN; VISUAL	ARRESTIN,	DESENSITISATION OF THE	VISUAL TRANSDUCTION 2	CASCADE, BINDING TO	ACTICATED AND PHOSPHORYLATED
	Compound		ARRESTIN; CHAIN: A, B, C, D;							ARRESTIN; CHAIN: A, B, C, D;									ARRESTIN; CHAIN: A, B, C, D;							
Table 5	SEQ FOLD score		•							52.32																
Та	PMF		0.22																0.29							
	Verify score		-0.03																0.16							
ļ	Psi Blast		1.5e-48							1.5e-48									1.5e-48							
	END		241						, ,	336									241							
	START AA		16																16							
	CHAIN ID		А							<u> </u>									Ω				•			
	PDB ID		lcfi						1	lctl			*						lcfi							
	SEQ ID NO:		1197						_	1197								\neg	1197							

	PDB annotation	RHODOPSIN	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE		SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION	SOS, PLECKSTRIN HOMOI OGY OH NOWAN	TRANSFERASE GRK-2,	BETA-ADRENERGIC RECEPTOR KINASE 1. BFTA-	ARK PLECKSTRIN	HOMOLOGY DOMAIN, PH	DOMAIN, SIGNAL	TRANSDUCTION, 2 G-BETA-	GAMMA BINDING DOMAIN,	BETA-ADRENERGIC	RECEPTOR 3 KINASE, BETA-	ARK, G-PROTEIN COUPLED	RECEPTOR KINASE (GRK-2)	EXCHANGE FACTOR B2-1,	SEC7 HOMOLOG B2-1;	EXCHANGE FACTOR,	INTEGRIN BINDING	PROTEIN	EXCHANGE FACTOR B2-1,
	Compound		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;		SOS1; CHAIN: NULL;		G-PROTEIN COUPLED	NULL;										CYTOHESIN-1; CHAIN: NULL;				CVTOTIFICE 1 OTT 1 THE TANK THE	CYTORESIN-1; CHAIN: NOLL;
Table 5	SEQ FOLD score							_										294.37					
Ta	PMF		0.76		0.01		-0.08															1 00	1.00
	Verify score		-0.42		0.19		0.04															0 60	200
	Psi Blast		8.4e-05		1.2e-05		1e-10	_			,						1 1. 07	1.1e-8/				1 16-87	1000
1	END		709		343		369										256					247	1
E	SIAKI AA		674		/ 47		255	_								_	25					57	
-	CEAIN		A		-				_				_					*				43	
תחת	L D		1161		iawe e		1 bak					- 14					11,00					1bc9	
OED	A D S		1202	1217	1214		1214										1214					1214	<u> </u>

	PDB annotation	SEC7 HOMOLOG B2-1; EXCHANGE FACTOR, INTEGRIN BINDING PROTEIN	EXCHANGE FACTOR B2-1, SEC7 HOMOLOG B2-1; EXCHANGE FACTOR, INTEGRIN BINDING	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GENE	SIGNALING PROTEIN ARFI GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN	SIGNALING PROTEIN ARFI GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN	EXCHANGE FACTOR ARE NUCLEOTIDE-BINDING SITE OPENER; EXCHANGE FACTOR, SEC7, ARNO, ARF FUNCTIONAL CLASS: GUANINE 2 NUCLEOTIDE	EXCHANGE FACTOR ARF NUCLEOTIDE-BINDING SITE
	Compound		CYTOHESIN-1; CHAIN: NULL;	HUMAN SOS 1; CHAIN: A;	GRP1; CHAIN: A;	GRP1; CHAIN: A;	ARNO; CHAIN: NULL;	ARNO; CHAIN: NULL;
Table 5	SEQ FOLD score						319.44	
Tal	PMF		1.00	0.10	1.00	1.00		1.00
	Verify		0.81	-0.24	0.35	0.01		1.00
	Psi Blast		8.5e-50	6.8e-18	4.8e-35	1.7e-19	3.6e-91	3.6e-91
	END		250	343	355	354	246	246
	START		57	33	256	265	52	52
	CHAIN		,	A	A	A		
	PDB ID		1bc9	1dbh	1fgy	1fgy	1pbv	1pbv
	SEQ NO:		1214	1214	1214	1214	1214	1214

	PDB annotation	OPENER; EXCHANGE FACTOR, SEC7, ARNO, ARF FUNCTIONAL CLASS: GUANINE 2 NUCLEOTIDE	EXCHANGE FACTOR EXCHANGE FACTOR ARF NUCLEOTIDE-BINDING SITE OPENER; EXCHANGE FACTOR, SEC7, ARNO, ARF FUNCTIONAL CLASS: GUANINE 2 NUCLEOTIDE	EXCHANGE FACTOR SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION	ENDOCYTOSIS/EXOCYTOSI S SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDI E		
	Compound		ARNO; CHAIN: NULL;	SOS 1; CHAIN: NULL;	SYNTAXIN-1A; CHAIN: A, B, C;	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3
Table 5	SEQ FOLD score						
Tal	PMF		1.00	0.51	0.39	-0.01	0.42
	Verify		1.05	0.14	0.06	0.18	-0.03
	Psi Blast		5.1e-48	8.5e-06	0.0004	6.8e-13	3.4e-13
	END		246	343	148	250	274
	START		56	247	12	52	11
	CHAIN				A		
444	FDB ID		1pbv	1pms	1ez3 ,	lgof	lgof
S. C.	NO B		1214	1214	1217	1226	1227

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ממת	PDB annotation	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE,	PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	SIGNALLING COMPLEX RAC1; P67PHOX;	SIGNALLING COMPLEX,	GIFASE, NADPH UXIDASE, PROTEIN-PROTEIN 2	COMPLEX, TPR MOTIF	SIGNALLING COMPLEX RAC1; P67PHOX;	SIGNALLING COMPLEX,	GTPASE, NADPH OXIDASE,	PROTEIN-PROTEIN 2	SIGNALLING COMPLEY	RAC1; P67PHOX;	SIGNALLING COMPLEX,	GTPASE, NADPH OXIDASE,	PROTEIN-PROTEIN 2	COMPLEX, TPR MOTIF	CHAPERONE HOP, TPR-	DOMAIN, PEPTIDE-	COMPLEX, HELICAL	REPEAT, HSP90, 2 PROTEIN BINDING
	Compound	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A;	NEUTROPHIL CYTOSOL	FACTOR 2 (NCF-2) CHAIN: B;		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A;	NEUTROPHIL CYTOSOL	FACTOR 2 (NCF-2) CHAIN: B;		RAS-RET ATED C3 BOTTII INITM	TOXIN SUBSTRATE 1; CHAIN: A;	NEUTROPHIL CYTOSOL	FACTOR 2 (NCF-2) CHAIN: B;			TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-PEPTIDE	MEEVD; CHAIN: B;	
Table 5	SEQ FOLD score										-										
Ta	Score	0.24		0.30				-0.15				-0.09						0.34			
Verify	score	0.25		-0.25				-0.00				90.0						0.37			
De:	FSI	1.2e-07		1.2e-08				5.1e-13				1.7e-14						3.4e-22			
FNT	AA	256		129				378				188						150			
START	AA	98		_				224				37						32			
CHAIN				В				B				В						Ą			
PDR		la17		1e96				1e96				1e96						lelr			
SEO	A S	1231		1231				1231				1231						1231		,,,,	

WO 03/029271 PCT/US02/30474 681

	PDB annotation	CHAPERONE HOP, TPR- DOMAIN, PEPTIDE- COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70,	CHAPERONE HOP, TPR- DOMAIN, PEPTIDE- COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTTEN RINDING	CHAPERONE HOP, TPR- DOMAIN, PEPTIDE- COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70,	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
	Compound	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP, CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;
Table 5	SEQ FOLD	2000				
Ta	PMF	09.0	0.04	-0.14	-0.17	-0.06
	Verify	0.26	0.28	0.05	-0.00	0.19
	Psi Blast	8.5e-20	1.7e-08	5.1e-09	5.1e-09	1.7e-37
	END	141	115	196	120	309
	START AA	32	4	71	15	38
	CHAIN	A	¥.	A	A	A
	PDB ID	lelw	lelw	lelw	1fch	1fch
	SE G SE	1231	1231	1231	1231	1231

	PDB annotation	REPLICATION DNA NUCLEOTIDE EXCISION	REPAIR, UVRABC,	HELICASE, 2 HYPERTHERMOSTABLE	PROTEIN	HYDROLASE UVRB;	GENE REGULATION APO	PROTEIN	TRANSLATION YEAST	ETF4A: HFI ICASE	TAITTA TION EACTOR AA	DEAD-BOX PROTEIN	TRANSLATION	EUKARYOTIC INITIATION	FACTOR 4A; IF4A,	HELICASE, DEAD-BOX	PROTEIN		CALCIUM-BINDING	CALCIUM++/PHOSPHOLIPID	BINDING PROTEIN, 2	CALCITIM-BINDING	PROTEIN	OXIDOREDUCTASE PDZ	DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
	Compound	DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN:	A;			EXCINUCLEASE ABC SUBUNIT B: CHAIN: A:	EXCINUCLEASE UVRABC	COMPONENT UVRB; CHAIN: A;	EUKARYOTIC INITIATION	racion 44, cirdin. A,			YEAST INITIATION FACTOR 4A;	CHAIN: A, B;					PROTEIN KINASE C (BETA);	CIRALIY, A, B,	•			NEURONAL NITRIC OXIDE	SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;
Table 5	SEQ FOLD score																								
Tal	PMF	68.0				0.71	0.43		1.00				0.84					,	00:1					66.0	
	Verify	0.42		b.		0.40	-0.25		0.58				0.04					000	0.08					66.0	
	Psi Blast	5.1e-21				3.4e-21	1e-24		1.7e-43				5.1e-66					9	5.4e-48					1.2e-15	
	END	253				256	272		258				258						1123					871	
- 1	START	92				92	22		104										983					008	
	CHAIN	Ą		_		А	A	Ţ	¥				В						W.					A	
	PDB	1c40	_			1d2m	1d9x		1 fuk				1 fuu					1.05	[778]					1b8q	
	SEQ NO:	1248			\rightarrow	1248	1248		1248				1248			·.		1050	5621					1253	

																,						
	PDB annotation	PEPTIDE RECOGNITION, PEPTIDE RECOGNITION,	ENDOCYTOSIS/EXOCYTOSI	S SYNAPTOTAGMIN, C2- DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2	RELEASE, ENDOCYTOSIS/EXOCYTOSI	HYDROLASE CPLA2;	PHOSPHOLIPASE, LIPID- BINDING HYDROI ASF	LIPID DEGRADATION PLC-	DI; PHOSPHORIC DIESTER HYDROLASE HYDROLASE	LIPID DEGRADATION, 2	TRANSDUCER, CALCIUM-	BINDING, PHOSPHOLIPASE	C, 3 FHOSPHOINOSI IIDE- SPECIFIC	ENDOCYTOSIS/EXOCYTOSI	S BETA SANDWICH,	CALCIUM ION, C2 DOMAIN	ENDOCYTOSIS/EXOCYTOSI	S BETA SANDWICH,	CALCIUM ION, C2 DOMAIN	TRANSFERASE CALCIUM++,	PHOSPHOLIPID BINDING	FROI EIN, CALCIUM- BINDING 2 PROTEIN.
	Compound	PSD-95; CHAIN: A; CRIPT; CHAIN: B;	SYNAPTOTAGMIN I; CHAIN: A;			CYTOSOLIC PHOSPHOLIPASE	A2; CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC	rnosrnolirase C, Chain: A, B;					SYNAPTOTAGMIN III; CHAIN: A;		TO THE TOTAL TAXABLE T	SYNAPTOTAGMIN III; CHAIN: A;			PROTEIN KINASE C, ALPHA	IIIE, CIMIN. A;	
Table 5	SEQ FOLD			•											-		_				-	
Та	PMF score	0.72	1.00			0.09		0.87						0.49		5	 00:1			7.00		
	Verify score	-0.05	0.14			0.05		0.21						0.02		0.45	0.45			0.14		
	Psi Blast	9.6e-11	6.8e-50			9.6e-26		8.4e-21						3.4e-21		1 50 A2	1.36-43		1 7. 50	1./6-52		
	END	068	1119			1126		1119						1121		1125	717		1104	1124		
	START	828	983			994		666						981		080	702		000	706		
	CHAIN	A	А			A		g	_					A		A			V	ς		
	PDB ID	1be9	1byn			1cjy	;	ldjx		-			-	Iddv		1day	À		1 dev			
	SEQ NO:	1253	1253			1253		1253					200	5521		1253	CCTT	<u>-</u>	1253	777		

WO 03/029271 PCT/US02/30474 684

	PDB annotation	PHOSPHATIDYLSERINE, PROTEIN KINASE C	CYTOKINE LCF; CYTOKINE,	LYMPHOCYTE CHEMOATTRACTANT	FACTOR, PDZ DOMAIN	SIGNAL TRANSDUCTION	HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION,	SH3 DOMAIN, REPEAT	OXIDOREDUCTASE BETA-	FINGER					ENDOCYTOSIS/EXOCYTOSI S C2-DOMAINS, C2B-	DOMAIN, RABPHILIN,	ENDOCYTOSIS/EXOCYTOSI S	ENDOCYTOSIS/EXOCYTOSI	S C2-DOMAINS, C2B-	DOMAIN, KABFRILLIN,	ENDOCYTOSIS/EXOCYTOSI	2		CALCIUM-BINDING	CALCIUM++/PHOSPHOLIPID
	Compound		INTERLEUKIN 16; CHAIN: NULL;			HUMAN DISCS LARGE	PROTEIN; CHAIN: NULL;		NEURONAL NITRIC OXIDE	SYNTHASE (RESIDUES 1-130); CHAIN: A;	CALCIUM/PHOSPHOLIPID	BINDING PROTEIN	SYNAPTOTAGMIN I (FIRST C2	DOMAIN) (CALB) 1RSY 3	RABPHILIN 3-A; CHAIN: A;			RABPHILIN 3-A; CHAIN: A;						PROTEIN KINASE C (BETA);	OLIMIN. A, B,
Table 5	SEQ FOLD score																			_					
Ta	PMF		0.92			60.0			0.34		1.00				0.99			1.00						1.00	
	Verify score		0.59			0.30			0.12		0.01				0.24			0.19						0.11	
	Psi Blast		1.1e-16			4.8e-13			4.8e-16		1.7e-49				1.2e-26			4.8e-29					,	5.1e-51	
	END		928			098			868		1117				1122		!	1119					, , , ,	1114	
	START		008			008			199		883				985			986					000	983	
	CHAIN								Ą						А			A						∢	
	PDB		li16			1pdr			1dan		lrsy				3rpb			3rpb						1a25	
	S B B S B S		1253			1253			1253	!	1253				1253			1253					,,,,,,	1254	

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	PDB annotation	BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN I OCALIZATION	ENDOCYTOSIS/EXOCYTOSI S SYNAPTOTAGMIN, C2- DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSI	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID- BINDING, HYDROLASE	LIPID DEGRADATION PLC- D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM- BINDING, PHOSPHOLIPASE
	Compound		PROTEIN KINASE C (BETA); CHAIN: A, B;	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B:	PSD-95; CHAIN: A; CRIPT; CHAIN: B;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;
Table 5	SEQ FOLD score		94.21					
Та	PMF			66.0	0.72	1.00	0.17	0.81
	Verify score			0.99	-0.05	0.40	0.02	0.23
	Psi Blast		5.1e-51	1.2e-15	9.6e-11	1.5e-52	1.2e-26	6e-23
	END		1117	871	068	1110	1117	1110
	START		983	800	828	983	994	666
	CHAIN		¥	А	A	A	A	м
	PDB		1a25	1b8q	1be9	1byn	Icjy	1djx
	SEQ NO:		1254	1254	1254	1254	1254	1254

										_																			_	
	PDB annotation		C, 3 PHOSPHOINOSITIDE- SPECIFIC	ENDOCYTOSIS/EXOCYTOSI	S BETA SANDWICH,	CALCIUM ION, C2 DOMAIN	ENDOCYTOSIS/EXOCYTOSI	S BETA SANDWICH,	CALCIUM ION, C2 DOMAIN	TRANSFERASE CALCIUM++,	PROTEIN CALCITIN	INOIDIN, CALCACIME	BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE,	PROTEIN KINASE C	CYTOKINE LCF; CYTOKINE,	LYMPHOCYTE	CHEMOATTRACTANT	FACTOR, PDZ DOMAIN	SIGNAL TRANSDUCTION	HDLG, DHR3 DOMAIN;	SIGNAL TRANSDUCTION,	SH3 DOMAIN, KEPEAI	OXIDOREDUCTASE BETA-	FINGER					ENDOCYTOSIS/EXOCYTOSI S C2-DOMAINS, C2B-
	Compound			SYNAPTOTAGMIN III; CHAIN: A;			SYNAPTOTAGMIN III; CHAIN: A;			PROTEIN KINASE C, ALPHA	int, circuit A,					INTERLEUKIN 16; CHAIN: NULL;				HUMAN DISCS LARGE	PROTEIN; CHAIN: NULL;			NEURONAL NITRIC OXIDE	SYNTHASE (RESIDUES 1-130); CHAIN: A:	CALCIUM/PHOSPHOLIPID	BINDING PROTEIN	SYNAPTOTAGMIN I (FIRST C)	DOMAIN) (CALB) 1RSY 3	RABPHILIN 3-A; CHAIN: A;
Table 5	SEQ FOLD	score																												
Ta	PMF			0.87			1.00			1.00						0.92				60.0				0.34		1.00				1.00
	Verify			0.22			0.47			0.03						0.59				0.30				0.12		0.53				0.23
	Psi Blast			1e-23			6.8e-45			1.7e-54						1.1e-16				4.8e-13				4.8e-16		5.1e-52				1e-30
	END			1109			1116			1115						928				098				868		1108				1113
	START AA			981			984			286						800				008				66/		983				985
	CHAIN			A			A			¥.														A						А
	PDB ID			ldqv			ldqv			ldsy						1i16	-			1pdr				lgau	~	lrsy				3rpb
	SEQ ED SE	Ž.		1254			1254			1254						1254				1254			1,00,	1254		1254				1254

			-γ																
	PDB annotation	DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSI S	ENDOCYTOSIS/EXOCYTOSI S C2-DOMAINS, C2B- DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSI S		CONTRACTILE PROTEIN TROPOMYOSIN COILED-	COLL ALFRA-HELICAL, CONTRACTILE PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF	SPECTRIN, ALPHA HELICAL	TANDEM 3-HELIX COILED-	COILS, STRUCTURAL PROTFIN	STRUCTURAL PROTEIN	TWO REPEATS OF	SPECTRIN, ALPHA HELICAL	LINKER REGION, 22	TANDEM 3-HELIX COILED-	COILS, STRUCTURAL	STRUCTURAL PROTEIN	TWO REPEATS OF	SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2
	Compound		RABPHILIN 3-A; CHAIN: A;		TROPOMYOSIN; CHAIN: A, B, C, D		ALPHA SPECTRIN; CHAIN: A, B, C;				ALPHA SPECTRIN; CHAIN: A, B,	ť					ALPHA SPECTRIN; CHAIN: A. B.	Ú	
Table 5	SEQ FOLD score																		
Ta	PMF		1.00		0.15		-0.06				-0.13						0.54		
	Verify score		0.51		-0.68		0.10				0.11						0.09		
	Psi Blast		3.6e-31		3.4e-26		3.6e-19				1.2e-15						2.4e-18		
	END		1110		981		1554				1592						245		
	START		986		989		1345				1377						20		
	CHAIN		A		∢		A				A						A	=	
	PDB		3rpb	,	lclg		Tom				1cun	-			•••		1cun		
	SEQ PO PO PO PO PO PO PO PO PO PO PO PO PO		1254	0,0	6071	0	6271				1259						1259		

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	PDB annotation		TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN	TWO REPEATS OF	SPECTRIN, ALPHA HELICAL LINKER REGION. 22	TANDEM 3-HELIX COILED-	COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN	TWO REPEATS OF	SPECTRIN, ALPHA HELICAL	LINKER REGION, 22	TANDEM 3-HELIX COILED-	COILS, STRUCTURAL	PROTEIN	STRUCTURAL PROTEIN	TWO REPEATS OF	SPECTRIN, ALPHA HELICAL	LINKER REGION, 22	TANDEM 3-HELIX COILED-	COILS, STRUCTURAL	PROTEIN	STRUCTURAL PROTEIN	TWO REPEATS OF	SPECTRIN, ALPHA HELICAL	LINKER REGION, 22	TANDEM 3-HELIX COILED-	COILS, STRUCTURAL PROTEIN
	Compound			ALPHA SPECTRIN; CHAIN: A, B,	ပ်				ALPHA SPECTRIN; CHAIN: A, B,	Ċ;						ALPHA SPECTRIN; CHAIN: A, B,	ပ်						ALPHA SPECTRIN; CHAIN: A, B,	Ú				
Table 5	SEQ FOLD	score																•										
Ta	PMF			0.22					-0.03				-			-0.07				_			0.24					
	Verify score			0.01					0.17							0.01							0.15					
	Psi Blast			9.6e-12					2.4e-09							9.6e-16							3.6e-14					
ļ	END			471					626							1118	•						321					
	START AA			255					292							918							97					
	CHAIN			A					А							А							¥					
	PDB ID			1cun					1cun							1cun							lcun					
	SEQ D	NO:		1259					1259							1259							1259					

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	PDB annotation		ENDOCYTOSIS/EXOCYTOSI S NSEC1; PROTEIN-PROTEIN	ENDOCYTOSIS/EXOCYTOSI	S NSEC1; PROTEIN-PROTEIN	ENDOCYTOSIS/EXOCYTOSI	S NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	MEMBRANE PROTEIN FOUR	HELIX BUNDLE, ALPHA	HELIX	MEMBRANE PROTEIN FOUR	HELIX BUNDLE, ALPHA	HELIX	CHAPERONE ARCHAEAL	PROTEIN	CONTRACTILE PROTEIN	TRIPLE-HELIX COILED	PROTEIN	CONTRACTILE PROTEIN	TRIPLE-HELIX COILED	COLL, CONTRACTILE PROTFIN	COMPLEX	(TRANSFERASE/PEPTIDE)	(TRANSFERASE/PEPTIDE),
!	Compound		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B.	SYNTAXIN BINDING PROTEIN 1:	CHAIN: A; SYNTAXIN 1A;	SYNTAXIN BINDING PROTEIN 1:	CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SSO1 PROTEIN; CHAIN: A;			SSO1 PROTEIN; CHAIN: A;			PREFOLDIN; CHAIN: A;	PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	HUMAN SKELETAL MUSCLE	ALPHA-ACTININ 2; CHAIN: A;		HUMAN SKELETAL MUSCLE	ALPHA-ACTININ 2; CHAIN: A;		SYK KINASE; CHAIN: A, C, E, G,	I, K; T-CELL SURFACE	CHAIN; CHAIN: B, D, F, H, J, L;
Table 5	SEQ	FOLD														-							59.55		
Ta	PMF	score	0.23	0.36		0.59			0.49			0.00			90.0		0.03			0.07					
	Verify	score	-0.05	-0.03		0.15			0.14			-0.08			0.10		-0.17			-0.38					
	Psi	Blast	1.2e-09	4.8e-13		1.2e-11			1.1e-07			2.4e-11			8.5e-08		4.8e-19			3.6e-18			1.7e-18		
	EZE:	AA	1729	546		582			376			964			104		1709			472			441		
	START	AA	1509	365		382		0	188			765			13		1447			172			222		
	CHAIN	<u> </u>	В	В		В			A			A			A		A			A			E		
	PDB	CIT	1dn1	1dn1		1dn1		į	lfio			1fio			1fxk		1duu	***		lquu			1a81		
	SEQ	NÖ NÖ	1259	1259		1259			1259			1259			1259		1259			1259			1261		

	PDB annotation		SYK, KINASE, SH2 DOMAIN, ITAM																	SH2 DOMAIN	PHOSPHATIDYLINOSITOL 3-	KINASE REGULATORY	ALPHA SH2 DOMAIN,	P85ALPHA, PI 3-KINASE,	NMR, C TERMINAL SH2 2	DOMAIN	TRANSFERASE
	Compound			TRANSFERASE(PHOSPHOTRANS FERASE) PROTO-ONCOGENE	TYROSINE KINASE	(E.C.E. / IIIIZ) 19BZ 3 (SRC) HOMOLOGY 2 DOMAIN)	("ABELSON", SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	TRANSFERASE(PHOSPHOTRANS	FERASE) PROTO-ONCOGENE	TYROSINE KINASE	(E.C.2./1.112) IAB2 3 (SRC)	HOMOLOGI Z DOMAIN)	(NMR, 20 STRUCTURES) 1AB2 5	HYDROLASE(SH2 DOMAIN)	TYROSINE PHOSPHATASE SYP	(N-TERMINAL SH2 DOMAIN)	1AYA 3 (PTP1D, SHPTP2)	(E.C.3.1.3.48) COMPLEXED WITH	THE PEPTIDE 1AYA 4 PDGFR- 1009 1AYA 5	P85 ALPHA; CHAIN: NULL;							NICOTINATE
Table 5	SEQ	FOLD		59.80																							
Ta	PMF	score						0.57						0.99						96.0							-0.15
	Verify	score						65.0						0.54						0.22							0.31
	Psi	Blast		1.2e-23				1.2e-23						7.2e-22						4.8e-22	-		-				2.4e-08
	END	AA		441				438						436						436							193
	START	AA		331				339						339			,,			336							5
	CHAIN	A											1	A													A
	PDB	A		lab2				1ab2						laya						1bfi					1		1d0s
	SEO	A Ö		1261				1261						1261						1261							1261

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	PDB annotation		DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE	SH2 DOMAIN GRB2, GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE	COMPLEX (KINASE/PEPTIDE)	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE		HORMONE/GROWTH FACTOR GRB2-SH2; SIGNAL TRANSDUCTION, SH2
	Compound		MONONUCLEOTIDE:5,6- CHAIN: A;	GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	P56—LCK— TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	GROWTH FACTOR RECEPTOR BINDING PROTEIN; CHAIN: E; SHC-DERIVED PEPTIDE; CHAIN:
Table 5	SEQ FOI D	score							
Tak	PMF	score		1.00	0.05	0.48	-0.20	-0.19	0.95
	Verify	score		0.21	0.28	0.16	1.24	1.98	0.50
	Psi	Blast		6e-22	5.1e-24	1.7e-22	6е-08	3.6e-08	9.6e-22
	CNA S	AA		436	432	436	99	19	436
	START	AA		334	281	283	4	5	338
	CHAIN					A	∢		田
	PDB	 A		1fhs	1 fmk	11ck	10sm	1pho	lqg1
	SEQ	A Ś		1261	1261	1261	1261	1261	1261

	PDB annotation		DOMAIN, PHOSPHOTYROSYL PEPTIDE, 2 COMPLEX	(SIGNAL TRANSDUCTION/PEPTIDE), HORMONE/GROWTH	FACTOR	TRANSFERASE TRANSFERASE, TYROSINE	KINASE, SH3, SH2, ONCOPROTEIN	TRANSFERASE TRANSFERASE, TYROSINE	KINASE, SH3, SH2, ONCOPROTEIN				HYDROLASE TETRATRICOPEPTIDE, TRP;	HYDROLASE, PROTEIN-	PROTEIN INTERACTIONS,	TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	CHAPERONE CHAPERONE,	
	Compound		Ţ.			ABL TYROSINE KINASE; CHAIN: NULL:		ABL TYROSINE KINASE; CHAIN:	NOLL,	SIGNALLING PROTEIN PHOSPHATIDYLINOSITOL 3-	KINASE (E.C.2.7.1.137) (N- TERMINAL 2PNA 3 SH2 DOMAIN	OF P85-ALPHA SUBUNIT) (NMR, 22 STRUCTURES) 2PNA 4	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;				PROGESTERONE RECEPTOR	F25; CFAIN: A, D,
Table 5	SEQ	roll score				64.01		Ē										
Tab	PMF	score			.,			0.19		06:0			09.0				98.0	
	Verify	score						0.01		0.20			-0.35				0.33	
	Psi	Blast			_	8.5e-28		8.5e-28		2.4e-23			9.6e-13				1.2e-05	
	END	AA				437		437		436			350				83	
	START	AA				272		272		336			285				3	
	CHAIN	А			<u> </u>												A	
	PDB	A				2abl		2abl		2pna			1a17				1ejf	
	SEQ	日 う 日 う				1261		1261		1261			1263				1263	

	PDB annotation	SANDWICH	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR- LIKE REPEAT, PROTEIN TRANSPORT	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN	TRANSFERASE ALPHA- SUPERHELIX, TRANSFERASE	COMPLEX (TRANSDUCER/TRANSDUCT ION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCT ION)	CHRITCHT IN AT DROTTEN	SIRUCIORAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22
	Compound		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;		ALPHA SPECTRIN; CHAIN: A, B, C;
Table 5	SEQ FOLD score		73.19					
Tab	PMF score			-0.19	-0.20	-0.20		0.24
	Verify score			0.02	0.00	0.13		-0.31
	Psi Blast		4.8e-11	2.4e-08	4.8e-09	4.8e-10		1.2e-07
	END		339	190	501	452		417
	START		53	93	280	302		227
	CHAIN		A	A	A	<u>م</u>		А
	PDB ID		1qqe	1 quu	1qsa	2trc		1cun
	SEQ	ÖN.	1263	1263	1264	1264		1268

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	otation		TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN AT PHA HELICAL	N, 2.2	TANDEM 3-HELIX COILED-COILS. STRUCTURAL		STRUCTURAL PROTEIN	I WO KEFEALS OF SPECTRIN, ALPHA HELICAL	N, 22	TANDEM 3-HELIX COILED-	UKAL	CONTRACTILE PROTEIN	COILED							LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT,
	PDB annotation		TANDEM 3-HELIX CO COILS, STRUCTURAL PROTEIN	STRUCTURAL PRC TWO REPEATS OF SPECTRIN AT PHA	LINKER REGION, 22	TANDEM 3-HELIX CO	Z	STRUCTURAL PRO	EFEALS SIN, ALP	LINKER REGION, 22	M 3-HEI	COILS, STRUCTURAL PROTEIN	ACTILE	TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN							LIPID TRANSPORT A LIPOPROTEIN, LIPID TRANSPORT,
			TANDEM COILS, ST PROTEIN	STRUC TWO RI	LINKE	TANDE	PROTEIN	STRUC	SPECTI	LINKE	TANDE	COILS, ST PROTEIN	CONTR	TRIPLE-H COIL, COI	110011						LIPID TRANS LIPOPROTEN TRANSPORT
				: A, B,				i: A, B,					CLE	N: A;	DVI	ZI IZ	NA VED	MATE.	71177		IAIN:
	puno			I; CHAIN				I; CHAID					AL MUS	2; CHAD	TACELCI	TAGE) SI	UNE-TRI	DROXA	TYVOVI I		N A-I; CI
	Compound			PECTRIN				PECTRIN					SKELET	CTININ	TATTLE	NTHET/	.11) (SEF	RVI HV	S 4		PROTEI
				ALPHA SPECTRIN; CHAIN: A, B, C;				ALPHA SPECTRIN; CHAIN: A, B,	IJ				HUMAN SKELETAL MUSCLE	ALPHA-ACTININ 2; CHAIN: A;	TO A CIE/C	LIGASE(STNIRETASE) SERTE. TRNA SYNTHETASE	(E.C.6.1.1.11) (SERINE-TRNA	LIGASE) ISES 3 COME LEALE WITH SERVI -HYDROXAMATE-	AMP 1SES 4		APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;
; 5	SEQ FOLD	score		4				7 ,													
Table 5	PMF F			0.35			<u></u>	0.28					-0.17			9.04					-0.19
	Verify F											-						_			
	Ve			0.00				-0.01					0.01		\top	07:0-					0.10
	Psi Rlact	Diasi		2.4e-18				6e-12					2.4e-14		1000	0.0001	********				2.2e-09
	END	ŧ.		595				711					735		, ,	391					96
	START	4		374				456					526			320					5
	CHAIN			6				4						•					,		
	[E]			4				A					<	1	-	<u> </u>				-	A
	PDB	3		1cun				1cun					10mi	; ; ;	,	Ises					lavl
	SEQ	e ë		1268				1268					1268) 	,	1268					1274

	PDB annotation	CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	Compound		ALPHA SPECTRIN; CHAIN: A, B, C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;
Table 5	SEQ FOLD score						
Tal	PMF		-0.20	-0.20	-0.19	0.53	0.30
	Verify score		0.17	0.18	0.45	0.08	0.10
	Psi Blast		4.4e-09	2.2e-10	1.4e-16	8.5e-28	1.7e-23
	END AA		102	102	405	460	472
	START		6	6	302	382	409
	CHAIN		A	A	A	A	A
	PDB		1cun	1quu	1a1h	la1h	lalh
	SEQ EQ		1274	1274	1277	1277	1277

	PDB annotation	GENE REGULATION POZ DOMAIN; PROTEIN- PROTEIN INTERACTION	DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC	LEUKEMIA, GENE REGULATION	GENE REGULATION POZ DOMAIN; PROTEIN- PROTEIN INTERACTION	DOMAIN, TRANSCRIPTIONAL 2	REPRESSOR, ZINC-FINGER PROTEIN X-RAY	CRYSTALLOGRAPHY, 3	PROTEIN STRUCTURE,	LEUKEMIA, GENE	REGULATION GENE REGULATION POZ	DOMAIN; PROTEIN-	PROTEIN INTERACTION	TRANSCRIPTIONAL 2	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY
	Compound	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A:	Chain. A,			PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A:						PROMYELOCYTIC LEUKEMIA	ZINC FINGER PROTEIN PLZF;	CHAIN: A;		
Table 5	SEQ FOLD	score 65.70														
Tak	PMF					1.00						1.00				
	Verify score					90.0						0.63				
	Psi Blast	2.2e-23				6.8e-21						2.2e-23				
	END	142				134						142		-		
	START AA	20				23						23				
	CHAIN ID	A				A						4	!			
	PDB ID	1buo				1buo						15110				
	SEQ ID	NO:				1277	-,					1277	- -			

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	PDB annotation	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score					
Tat	PMF		-0.19	-0.18	99.0	0.28
	Verify score		0.15	0.33	0.41	-0.15
	Psi Blast		8.5e-27	6.8e-32	6.8e-46	6.8e-39
	END AA		349	405	460	473
	START AA		250	301	381	408
	CHAIN		O	U	U	O
	PDB ID		lmey	lmey	1mey	Imey
	SEQ EQ		1277	1277	1277	1277

	PDB annotation		STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA;	5S GENE; NMR, TFIIIA,	PROTEIN, DNA,	TRANSCRIPTION FACTOR,	5S RNA 2 GENE, DNA	BINDING PROTEIN, ZINC	FINGER, COMPLEX 3	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA POLYMERASE III, 2
	Compound			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN: E, F;								TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;	
Table 5	SEQ FOLD	score			_																								
Ta	PMF			-0.19					-0.13							-0.07										00.00			
	Verify score			0.73					0.18							0.21										0.43			
	Psi Blast			3.4e-09	•				1.2e-11						_	1.5e-15										3.4e-23			
	END			349					405							433										441			
	START			299					379							372										290			
	CHAIN			Ð					G							A										A			
	PDB			1mey			~		1mey							1463										1tf6			
	SEQ ED	NO:		1277					1277							1277										1277			

										_																		
	PDB annotation	TRANSCRIPTION INITIATION, ZINC FINGER	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) YING- VANG 1: TPANISCE EFFOR	INITIATION INITIATOR	ELEMENT VY1 ZINC 2	FINGER PROTEIN DNA-	PROTEIN RECOGNITION 3	COMPLEY (TRANSCOUNTION, 3	COMPLEA (IRANSCRIPTION PEGITA ATTONIA)	COMPLEY (TP ANSCRIPTION)	DECIM ATOMESTANDED	NEGOLATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	TRANSCRIPTION REGIL ATTON
	Compound		TFIIIA; CHAIN: A, D; 5S	KIBOSOMAL RNA GENE; CHAIN: R C F F:	ت, ر, بے, ۲,				VANTA CALLES OF THE CALLES	ASSOCIATED VIBITS BE	INITIATOR FLEMENT DNA:	CHAIN: A. B.						YY1; CHAIN: C: ADENO-	ASSOCIATED VIRIS DS	NITIATO EL EMENT DALA	CITY TO THE PROPERTY OF THE PR	CHAIN: A, B;						ADR1; CHAIN: NULL;
Table 5	FOLD score																											
I a	score		0.00						0.01	0.21					,			0.22									,	-0.17
Verify	score		0.14						0.33								İ	-0.33									i,	0.57
Pei	Blast		1.7e-25						6 Re-27	7								1.5e-26	-								00	8.3e-09
END	AA		473						460	}	-							468	•								407	101
START	AA		372						372				-	0				388								•	37/4	+ 1
CHAIN	А		A		·		_		S										-	_								
PDB	О		1466						lubd						•		\dashv	pqnI			_						2adr	
SEQ	A Ö		1277						1277									1/71									1277	\neg

	PDB annotation	TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	Calculate a Con- 10 Grant Head	HYDROLASE CATALYTIC MECHANISM, METALLOENZYME, PROTEIN PHOSPHATASE 2C, 2 SIGNAL TRANSDUCTUIN, X-RAY CRYSTALLOGRAPHY, HYDROLASE	HYDROLASE CATALYTIC MECHANISM, METALLOENZYME, PROTEIN PHOSPHATASE 2C, 2 SIGNAL TRANSDUCTUIN, X-RAY CRYSTALLOGRAPHY, HYDROLASE
	Compound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;		PHOSPHATASE 2C; CHAIN: NULL;	PHOSPHATASE 2C; CHAIN: NULL;
Table 5	SEQ FOLD	21026				54.51	
Tat	PMF		-0.20	-0.13			1.00
	Verify score		0.31	0.22			-0.04
	Psi Blast		5.16-19	1.4e-23		8.5e-65	8.5e-65
	END		404	432		445	451
	START AA		283	343		72	83
	CHAIN		A	A			
	PDB ID		2gli	2gli		1а69	1a6q
	SEQ	.0X	1277	1277		1287	1287

	PDB annotation	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE	TRANSFERASE HRS: HRS.	VHS, FYVE, ZINC FINGER, SUPERHELIX	TRANSFERASE HRS, VHS, FYVE, ZINC FINGER, SUPERHELIX	TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF
	Compound	NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	INVASIN; CHAIN: A;	HEPATOCYTE GROWTH	FACTOR-REGULATED TYROSINE CHAIN: A;	HEPATOCYTE GROWTH FACTOR-REGULATED TYROSINE CHAIN: A;	PHOSPHATIDYLINOSITOL-3- PHOSPHATE BINDING FYVE CHAIN: A;	ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;
Table 5	SEQ FOLD score		74.08						
Taf	PMF	-0.20		0.05	}	0.03	0.10	0.62	0.04
	Verify score	0.11		-0.91	·	-0.19	-0.80	-0.27	-0.08
	Psi Blast	80-99	2.2e-14	0.00017		1.2e-05	8e-06	2.2e-09	4.4e-13
	END	304	501	90	2	111	111	563	674
	START	81	7	33)	54	57	355	462
	CHAIN	A	А	V	4	¥	4	A	А
	PDB ID	1d0s	1cwv	1 drm	dan	1dvp	1vfy	1cun	1cun
	SEQ NO:	1291	1292	1203	C/71	1293	1293	1298	1298

F, F		_																								
PDB CHAIN START END Psi Verify PMF SEQ		PDB annotation		SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-	COILS, STRUCTURAL PROTEIN	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE	FROIEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA)	GABPALPHA; GABPBETA1;	REGULATION/DNA), DNA-	BINDING, 2 NUCLEAR	PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	IRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	GABPALPHA; GABPBETA1;	COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-	BINDING, 2 NUCLEAR	PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	GABPALPHA; GABPBETA1;
PDB		Compound				HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D. E:	``				A to the contract of the contr	GA BINDING PROTEIN ALPHA;	DDOTTEN DETA 1. CITABLE	FROIEIN BEIA I; CHAIN: B;	DIVA; CHAIN: D, E;						GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;
PDB CHAIN START END Psi Verify PM	ble 5	SEQ	FOLD																					73.20		
PDB CHAIN START END Psi	Ta	PMF	score			0.22		1.00						20.0	0.90				•			-				
PDB CHAIN START END		Verify	score			-0.19		0.27						0.10	0.10			-								
PDB CHAIN START AA AA AA AA AA AA AA		Psi	Blast			8.8e-24		6.8e-43						3 10 21	7.46-54									6.8e-43		
D DB CHAIN D DD Iquu A 4 Iawc B 1 Iawc B 3		END	AA A			681		252		•				290	707		•	****					100	18/		
DD I I I I I I I I I I I I I I I I I I		START	AA			443		105						138	2									54		
PDB Iquu Iquu Iawc Iawc Iawc		CHAIN	a			∢		B						В	1								-	Δ		
		PDB	3		-	Iquu		lawc				•		1awc) :			•					\dagger			
		SEQ	NO.		1000	8671		1299						1299	<u> </u>								+			

	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	IKANSCKIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TO ANGENTATION	COMPLEX (TRANSCRIPTION S FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TA ANSCRIPTION 3 EACTOR TO ANSCRIPTION 3 EACTOR	COMPLEX (TRANSCRIPTION STACTOR REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNABINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN.
	Compound	DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
Table 5	SEQ FOLD score				
Ta	PMF		1.00	1.00	0.92
9	veniy score		0.56	0.45	0.10
	FSI Blast		2.2e-38	1.4e-37	1.7e-36
T. C.	AA		186	186	153
CTADT	AA		36	38	٠,
CUAIN	CIPAIIN D		В	В	В
and	a a		lawc	lawc	lawc
OHO	Ž A Š		1299	1299	1299

	PDB annotation		ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA)	GABPALPHA; GABPBETA1;	COMPLEX (TRANSCRIPTION REGUL ATTON/DNA)	BINDING, 2 NUCLEAR	PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR.	CDK4/6 INHIBITOR.	ANKYRIN MOTIF	TUMOR SUPPRESSOR	TUMOR SUPPRESSOR,	CDK4/6 INHIBITOR,	ANKYKIN MOTIF	TUMOR SUPPRESSOR	TUMOR SUPPRESSOR,	CDK4/6 INHIBITOR,	ANK YKIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR	CDK4/6 INHIBITOR	ANKYRIN MOTIF	TUMOR SUPPRESSOR	TUMOR SUPPRESSOR,	CDK4/6 INHIBITOR,	THAIR I MIN IND I II.
	Compound			GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;					P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;			P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;			P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		DIODITION OF THE STATE OF THE S	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;			P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		
	SEQ FOLD	score												75.94														
	PMF score			1.00	_					,	0.96							7.00 1.00			5	1.00			1.00			
	Verify score			0.27						100	0.0							0.33			0.16	0.10			0.31			
	Psi Blast			8.5e-40						£ 1 - 71	J.16-31			6.6e-40			10.00	1.36-35			6 60 10	0.05-40			3.4e-33			
	END AA			219						220	667			190			107	10/			221	177			219			
	START			72						100	001			36			30	000			29	ò			75			
	CHAIN		,	x 1																						1		
	PDB ID		,	lawc						11,49	0000		5	spa i			11,40	nno	-		1148	2			1bd8			
) H	NO:	000	1299						1000	(7)		1200	6671	***		1200	6671			1299				1299			

Psi Verify PMF SEQ Compound PDB amotation
Table 5 Verify PMF SEQ Score Score FOLD Score 0.04 0.89 0.02 1.00 0.48 1.00
Tabl Verify PMF score score 0.04 0.89 0.04 0.09 0.04 0.48 1.00 0.48 1.00
Verify PM score scor 0.04 0.89 0.04 0.09 0.02 1.00
0 0
Psi Blast 6.6e-26 6.8e-31
END AA 221 225 255 255
START AA 102 36
CHAIN ID B B B
PDB Ibiz Ibix Ibix Ibix Ibix Ibix Ibix Ibix Ibix
SEQ ID NO: 1299 1299 1299 1299

-	PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR,
	Compound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;
	SEQ FOLD score		71.57			67.86
	PMF			1.00	0.84	
	Verify score			0.44	0.01	
	Psi Blast		1.16-39	1.2e-31	8.5e-39	8.5e-39
	END		224	219	257	229
	START		69	75	105	64
	CHAIN		В	В	Ą	A
	PDB		1blx	1blx	1bu9	1bu9
	SEQ Signal		1299	1299		1299

						
PDB annotation	P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH	FACTOR SIGNALING PROTEIN HELIX-TURN-HELIX,	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	CELL CYCLE NHIBITOR P18-NK4C(NK6); CELL CYCLE NHIBITOR, P18- NK4C(NK6), ANKYRIN REPEAT, 2 CDK 4/6	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT 2 CDK 4/6
Compound		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;
SEQ FOLD					71.13	
PMF		1.00	0.98	1.00		1.00
Verify score		0.29	0.14	0.15		0.06
Psi Blast		1.5e-34	5.1e-38	3.4e-29	5.1e-38	4.4e-35
END		191	256	263	223	221
STAKI		09	105	138	69	02
CHAIN		A	A	A	A	∢
TUB ID		1d9s	lihb	1 ihb	lihb	lihb
N B S				1299		1299
	ID ID AA AA Blast score score FOLD score	TD D AA AA Blast score Score FOLD score score	TDB CHAIN STAKT END PSI Verify PMF SEQ Compound Blast score score FOLD Score Score 1d9s A 60 191 1.5e-34 0.29 1.00 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	TDB CHAIN STAK1 END Psi Verify PMF SEQ Compound	The bound The	1d9s A 69 223 5.1e-38 1.15 A 60 191 1.5e-34 1.15

	PDB annotation		INHIBITOR	TRANSCRIPTION FACTOR	F65; F50D; TRANSCRIPTION	FACTOR, INB/INFINE COMPLEX	TRANSCRIPTION FACTOR	P65; P50D; TRANSCRIPTION	FACTOR, IKB/NFKB	COMPLEX	TRANSCRIPTION FACTOR	P65; P50D; TRANSCRIPTION	FACTOR, IKB/NFKB	COMPLEX	TRANSCRIPTION FACTOR	P65; P50D; TRANSCRIPTION	FACTOR, IKB/NFKB	COMPLEX	TRANSCRIPTION FACTOR	P65; P50D; TRANSCRIPTION	FACTOR, IKB/NFKB	COMPLEX	TRANSCRIPTION FACTOR	P65; P50D; TRANSCRIPTION	FACTOR, IKB/NFKB	COMPLEX	ANK-REPEAT	MYOTROPHIN,	ACETYLATION, NMR, ANK-	REPEAT	COMPLEX (TRANSCRIPTION REG/ANK REPEAT)
	Compound			NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAFFA-B F50D	ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-B-	ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-B-	ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-B-	ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-B-	ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-B-	ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL				NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-
Table 5	SEQ FOLD	score																	74.46								56.75				
Ta	PMF			0.15			0.82				0.72				1.00								1.00								1.00
	Verify score			-0.14			0.02				0.04				-0.11								-0.10								0.30
-	Psi Blast			3.4e-26			8.5e-39				1.2e-34				1.4e-45				6.6e-48				6.6e-48				1.3e-30				1e-39
	END			262			203				170				252				263				255				151			-	203
	START AA			133			33				2								89	****			69				35				32
	CHAIN		1	Ω			Q				Ω				Ω				Ω				a								E
	PDB ID			likn			1 iku				likn				lika				likn		7119];	likn L	_			lmyo		· · ·		1nfi
	SEQ ED SE			1299			1299				1299				1299				1299				1299				1299			,	1299

	PDB annotation		COMPLEX (TRANSCRIPTION	REGULATION/ANK	REPEAT), ANKYRIN 2	REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT)	COMPLEX (TRANSCRIPTION	REGULATION/ANK	REPEAT), ANKYRIN 2	REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT)	COMPLEX (TRANSCRIPTION	REGULATION/ANK	REPEAT), ANKYRIN 2	REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT)	COMPLEX (TRANSCRIPTION	REGULATION/ANK	REPEAT), ANKYRIN 2	REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT)	COMPLEX (TRANSCRIPTION	REGULATION/ANK	REPEAT), ANKYRIN 2	REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX (TRANSCRIPTION	מונון אורוסטויין אין אורוטווין וויסטווין
	Compound		KAPPA-B-ALPHA; CHAIN: E, F;			ATT IV A PRIA IN PACE CONT.	NF-KAPPA-B P65; CHAIN: A, C;	KADDA BATDHA: CHAIN: B, D; I-	INTERPORT OF THE PROPERTY OF T				NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D, I-	KAPPA-B-ALPHA; CHAIN: E, F;				NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D; I-	KAPPA-B-ALPHA; CHAIN: E, F;				NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D, I-	KAPPA-B-ALPHA; CHAIN: E, F;				NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P30; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E. F:	, , ,
Table 5	SEQ	FOLD																	75.28						-								
Ta	PMF	score				1 00	1.00					, ,	0.74 										-	5	 33:	•		•			1.00		
	Verify	score				0.50	00					11	-0.11											1.0	0.21						0.04		
	Psi	Blast				20-45	C+-07					1 75 34	1.25-74					10.40	1.8e-46					100 16	1.05-40				-	7 1 15	5.46-45		
		AA				326	077					170	2						70 7					255	(77					020			
	START	AA				39	ì					4	1					179	±					65	3					77			
1 2 2 2 2 2 2	CHAIN	E				E	<u> </u>					[II.	1		-			1	-					[T						LI C			
444	FUB E	3	 -			1nfi						1nf						1nfi						1nfi 1						1nfi I			
Cab) E	NO Si				1299				-		1299						1299	7	-				1299				_		1290			

	PDB annotation		REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES,	THIRD 2 N-TERMINAL DOMAIN	TRANSMEMBRANE,	GLYCOPROTEIN	CONNECTIN A71, CONNECTIN; TITIN,	CONNECTIN, FIBRONECTIN TYPE III	SIGNALING PROTEIN	CYTOKINE RECEPTOR,	GLYCOPROTEIN 130, GP130,	INTERCEURINE 0 2 DECENTOR DETA SIMILAR	SIGNALING PROTEIN	BINDING PROTEIN BINDING	PROTEIN, CYTOKINE	RECEPTOR	CELL ADHESION PROTEIN	RGD, EXTRACELLULAR	MATRIX 1FNF 18	CELL ADHESION PROTEIN	RGD, EXTRACELLULAR	MATRIX IFNF 18	HEPARIN AND INTEGRIN
	Compound			GP130; CHAIN: NULL;				TITIN; CHAIN: NULL;		GP130; CHAIN: A, B;					GRANULOCYTE COLONY-	STIMULATING FACTOR	RECEPTOR; CHAIN: NULL;	FIBRONECTIN; 1FNF 6 CHAIN:	NULL; 1FNF 7		FIBRONECTIN; 1FNF 6 CHAIN:	NULL; 1FNF 7		FIBRONECTIN; CHAIN: A;
Table 5	SEQ FOLD	score																						
Ta	PMF			0.49				90.0		0.12					-0.13			-0.14			0.42		,	0.16
	Verify score			0.13				0.24	i	0.14					0.01			0.32			0.38		;	0.11
	Psi Blast			6.6e-16				1.8e-16		0.00044					4.4e-16			1.3e-11		;	1.1e-13		,	0.6e-11
	END AA			452	·		!	457		457					452			481			452			481
	START			361			[357		359	•				353			356		0	359		0,00	303
	CHAIN									A	-												4	A
ŀ	PDB ID			1bj8				Ibpv		1bqu					lcto		,	Ħ		0	— 祖		1.01	umi
	S A S A	SQ:		1301			, , ,	1301		1301					1301		,00,	1301		1001	1301		1201	1301

	PDB annotation	BINDING HEPARIN AND INTEGRIN BINDING		CELL ADHESION PROTEIN,	KGD, EXIKACELLULAK MATRIX 2 HEPARN-	BINDING, GLYCOPROTEIN		CELL ADHESION PROTEIN,	MATRIX, 2 HEPARIN-	BINDING, GLYCOPROTEIN	UNIT; STRUCTURAL PROTEIN	INTEGRIN, HENTDESMOSOME	FIBRONECTIN.	CARCINOMA, STRUCTURAL	2 PROTEIN)NECTIN JLE)	S) 1TTF 3		FIBRONECTIN, TYPEIII	DOMAIN, ANGIOGENESIS,	PROTEIN 2 BINDING	\dashv	E; CHAIN: ENDONUCLEASE ENDONUCLEASE, TRNA	ENDONUCLEASE		EIN; TRANSCRIPTION ZINC
	Compound		FIBRONECTIN; CHAIN: NULL;				FIBRONECTIN; CHAIN: NULL;				INTEGRIN BETA-4 SUBUNIT;	CHAIN: A, B;				GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE)	(NMR, 36 STRUCTURES) 1TTF 3	FIBRONECTIN; CHAIN: A;					TRNA ENDONUCLEASE; CHAIN: A. B. C. D;			CREB-BINDING PROTEIN;
Table 5	SEQ FOLD score																									
Ta	PMF		0.27				0.55				-0.05					0.13		0.13					0.98			0.00
	Verify score		0.64				-0.01				0.33					0.13		0.28					-0.36			-0.90
	Psi Blast		4.4e-13				4.4e-12				2.2e-13					2.2e-15		1.5e-16					5.1e-06			0.0012
	END		452				524				452					452		448					169		!	232
	START AA		359				362				362					362		356					103			178
	CHAIN										A							A		_			Ą			A
	PDB		1mfn				1mfn				1qg3		•	•		1#f		2fnb					1a79			1f81
	SEQ NO.		1301		,		1301				1301					1301		1301					1306			1307

	PDB annotation	FINGER, TAZ2, CBP	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P, RIBOSOMAL PROTEIN L5P,
	Compound	CHAIN: A;	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;	23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL PROTEIN L5; CHAIN: D;
Table 5	SEQ FOLD score		63.71	62.50		
Tab	PMF				0.13	0.36
	Verify				-0.20	0.01
	Psi Blast		8.5e-09	6.6e-10	6.6e-10	6.8e-18
	END AA	-	337	321	324	79
	START AA		141	115	06	27
	CHAIN		A	⋖	<	M
	PDB ID		lavl	1cun	1cun	1ffk
	SEQ EQ	5	1309	1309	1309	1311

						_																											
	PDB annotation		HMAL5, HL13; 30S	RIBOSOMAL PROTEIN HS6;	50S KIBOSOMAL PROTEIN	L13P, HMAL13; 50S	RIBOSOMAL PROTEIN L14P,	HMAL14, HL27; 50S	RIBOSOMAL PROTEIN L15P,	HMAL15, HL9; 50S	RIBOSOMAL PROTEIN L18P,	HMAL18, HL12; 50S	RIBOSOMAL PROTEIN L18E,	HL29, L19; 50S RIBOSOMAL	PROTEIN L19E, HMAL19,	HL24; 50S RIBOSOMAL	PROTEIN L21E, HL31; 50S	RIBOSOMAL PROTEIN L22P,	HMAL22, HL23; 50S	RIBOSOMAL PROTEIN L23P,	HMAL23, HL25, L21; 50S	RIBOSOMAL PROTEIN L24P,	HMAL24, HL16, HL15; 50S	RIBOSOMAL PROTEIN L24E,	HL21/HL22; 50S RIBOSOMAL	PROTEIN L29P, HMAL29,	HL33; 50S RIBOSOMAL	PROTEIN L30P, HMAL30,	HL20, HL16; 50S RIBOSOMAL	PROTEIN L31E, L34, HL30;	50S RIBOSOMAL PROTEIN	L32E, HL5; 50S RIBOSOMAL	PROTEIN L37E, L35E; 50S
	Compound		RIBOSOMAL PROTEIN L7AE;	CHAIN: E; RIBOSOMAL	PROTEIN LI0E; CHAIN: F;	RIBOSOMAL PROTEIN L13;	CHAIN: G; RIBOSOMAL	PROTEIN L14; CHAIN: H;	RIBOSOMAL PROTEIN L15E;	CHAIN: I; RIBOSOMAL PROTEIN	L15; CHAIN: J; RIBOSOMAL	PROTEIN L18; CHAIN: K;	RIBOSOMAL PROTEIN L18E;	CHAIN: L; RIBOSOMAL	PROTEIN L19; CHAIN: M;	RIBOSOMAL PROTEIN L21E;	CHAIN: N; RIBOSOMAL	PROTEIN L22; CHAIN: 0;	RIBOSOMAL PROTEIN L23;	CHAIN: P; RIBOSOMAL PROTEIN	L24; CHAIN: Q; RIBOSOMAL	PROTEIN L24E; CHAIN: R;	RIBOSOMAL PROTEIN L29;	CHAIN: S; RIBOSOMAL PROTEIN	L30; CHAIN: T; RIBOSOMAL	PROTEIN L31E; CHAIN: U;	RIBOSOMAL PROTEIN L32E;	CHAIN: V; RIBOSOMAL	PROTEIN L37AE; CHAIN: W;	RIBOSOMAL PROTEIN L37E;	CHAIN: X; RIBOSOMAL	PROTEIN L39E; CHAIN: Y;	RIBOSOMAL PROTEIN L44E;
able 5	SEQ FOLD	score																															
Га	PMF score																																
	Verify score																					····											
	Psi Blast																																
	END	1				•																											
	START	1																															
	CHAIN	}																															
	PDB	3																															
	SEQ	ġ	5																													_	

_									.,																		-				7
	PDB annotation		RIBOSOMAL PROTEINS	L39E, HL39E, HL46E; 50S RIBOSOMAI PROTEIN 144F	I A HI A: 50S RIBOSOMAL	PROTEIN L6P, HMAL6, HL10	RIBOSOME ASSEMBLY,	RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN	RIBOSOME 50S RIBOSOMAL	PROTEIN L2P, HMAL2, HL4;	50S RIBOSOMAL PROTEIN	L3P, HMAL3, HL1; 50S	RIBOSOMAL PROTEIN L4E,	HMAL4, HL6; 50S	RIBOSOMAL PROTEIN L5P,	HMAL5, HL13; 30S	RIBOSOMAL PROTEIN HS6;	50S RIBOSOMAL PROTEIN	L13P, HMAL13; 50S	RIBOSOMAL PROTEIN L14P,	HMAL14, HL27; 50S	RIBOSOMAL PROTEIN L15P,	HMAL15, HL9; 50S	RIBOSOMAL PROTEIN L18P,	HMAL18, HL12; 50S	RIBOSOMAL PROTEIN L18E,	HL29, L19; 50S RIBOSOMAL	PROTEIN L19E, HMAL19,	HL24; 50S RIBOSOMAL	PROTEIN L21E, HL31; 50S REGROMAL PROTEIN 1,22P	ALDODOLINA LA
	Compound		CHAIN: Z; RIBOSOMAL	PROTEIN L6; CHAIN: 1;					23S RRNA; CHAIN: 0; 5S RRNA;	CHAIN: 9; RIBOSOMAL PROTEIN	L2; CHAIN: A; RIBOSOMAL	PROTEIN L3; CHAIN: B;	RIBOSOMAL PROTEIN L4;	CHAIN: C; RIBOSOMAL	PROTEIN L5; CHAIN: D;	RIBOSOMAL PROTEIN L7AE;	CHAIN: E; RIBOSOMAL	PROTEIN L10E; CHAIN: F;	RIBOSOMAL PROTEIN L13;	CHAIN: G; RIBOSOMAL	PROTEIN L14; CHAIN: H;	RIBOSOMAL PROTEIN L15E;	CHAIN: I; RIBOSOMAL PROTEIN	L15; CHAIN: J; RIBOSOMAL	PROTEIN L18; CHAIN: K;	RIBOSOMAL PROTEIN L18E;	CHAIN: L; RIBOSOMAL	PROTEIN L19; CHAIN: M;	RIBOSOMAL PROTEIN L21E;	CHAIN: N; RIBOSOMAL	INCIDIN DEE, CHAIN. V,
Table 5	SEQ	FOLD																													
Tak	PMF	score							0.22																						
	Verify	score							-0.14																						
	Psi	Blast							1.8e-24																						
	END	AA					-		79																						
	START	ΑA							29	ì																					
	CHAIN	А							2	í																					
	PDB	А							1ffk																					J.	
	SEQ	A S							1311	1																					

	PDB annotation		HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEINS L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10 RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD	TRANSCRIPTION INHIBITOR BETA-PROPELLER	TRANSCRIPTION INHIBITOR
	Compound		RIBOSOMAL PROTEIN L23; CHAIN: P; RIBOSOMAL PROTEIN L24; CHAIN: Q; RIBOSOMAL PROTEIN L24E; CHAIN: R; RIBOSOMAL PROTEIN L29; CHAIN: S; RIBOSOMAL PROTEIN L30; CHAIN: T; RIBOSOMAL PROTEIN L31E; CHAIN: U; RIBOSOMAL PROTEIN L32E; CHAIN: V; RIBOSOMAL PROTEIN L37AE; CHAIN: W; RIBOSOMAL PROTEIN L37E; CHAIN: X; RIBOSOMAL PROTEIN L39E; CHAIN: Y; RIBOSOMAL PROTEIN L44E; CHAIN: Z; RIBOSOMAL PROTEIN L56; CHAIN: 1;	TOLB PROTEIN; CHAIN: A;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR
Table 5	SEQ	rOLD score				
Ta	PMF	score		0.11	-0.12	0.93
	Verify	score		80.0	0.16	0.42
	Psi	Blast		0.0019	1.7e-41	1.7e-63
	END	AA		805	695	782
	START	AA		708	429	449
	CHAIN	JII		A	А	A
	PDB	∄		1crz	1erj	1erj
	SEQ	⊒ ÿ		1314	1314	1314

	PDB annotation		BETA-PROPELLER	TRANSCRIPTION INHIBITOR BETA-PROPELLER	COMPLEX (GTP.	BINDING/I KANSDUCEK) BETA1, TRANSDUCIN BETA	SUBUNIT; GAMMA1,	TRANSDUCIN GAMMA	SUBUNIT; COMPLEX (GTP-	BINDING/IKANSDUCEK), G	FROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-	BINDING/TRANSDUCER)	BETA1, TRANSDUCIN BETA	SUBUNII; GAMMAI,	TRANSDUCIN GAMMA	SUBUNIT; COMPLEX (GTP-	BINDING/TRANSDUCER), G	PROTEIN, HETEROTRIMER 2	SIGNAL TRANSDUCTION	COMPLEX (GTP-	BINDING/TRANSDUCER)	BELAI, IKANSDUCIIN BELA	SUBUNII; GAMMAI,	TRANSDUCIN GAMMA	SUBUNIT; COMPLEX (GTP-	BINDING/TRANSDUCER), G	PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	
	Compound		TUP1; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-ALPHA/GI-ALPHA CHIMERA;	CHAIN: A; G1-BE1A; CHAIN: B; GT-GAMMA; CHAIN: G;						GT-ALPHA/GI-ALPHA CHIMERA;	CHAIN: A; GT-BETA; CHAIN: B;	GT-GAMMA; CHAIN: G;							GT-ALPHA/GI-ALPHA CHIMERA;	CHAIN: A; GT-BETA; CHAIN: B;	GI-GAMIMA; CHAIN: G;						
Table 5	SEQ	FOLD			95.77																								
Tal	PMF	score		1.00								1.00									1.00								
	Verify	score		0.46								0.41									0.37								
	Psi	Blast		1.7e-48	1.4e-71							1.4e-71									3.4e-48								
	END	AA		805	779					-	•	622									804								
	START	AA		543	403							430									534								
	CHAIN	О		A	В							В									В								
	PDB	<u> </u>		1erj	1got							1got									lgot								
	SEQ	ВÄ		1314	1314							1314									1314								

	PDB annotation		TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE	OUTER MEMBRÂNE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE	SERINE PROTEASE SERINE				
	Compound		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	OMPK36; CHAIN: A, B, C;	ALPHA-LYTIC PROTEASE; CHAIN: A;	ALPHA-LYTIC PROTEASE;				
Table 5	SEQ	FOLD score								
Tal	PMF	score	-0.20	-0.19	-0.19	-0.20	-0.20	-0.20	-0.14	-0.19
	Verify	score	0.44	0.63	0.23	0.01	0.36	0.90	1.12	1.15
	Psi	Blast	1.1e-08	1.3e-20	1.8e-09	6.6e-10	1.8e-09	4.4e-16	4.4e-09	2.2e-09
	END	AA	170	365	290	740	136	238	157	156
	START	AA	2	20	228	378	S	9	13	2
	CHAIN	(II	A	A	A	A	A	A	A	
	PDB		1d0s	1d0s	1d0s	1d0s	1d0s	10sm	1994	1ta1
	SEQ	e ë	1318	1318	1318	1318	1318	1318	1318	1318

START END
Table 5 START END Psi Verify PMF SEQ AA AB Blast score FOLD score 13 235 8.8e-16 1.01 -0.20 26 363 1.3e-15 0.81 -0.19 413 744 4.4e-09 0.02 -0.17 19 97 1.4e-26 0.32 0.60
AA AA Blast score score score 13 235 8.8e-16 1.01 -0.20 26 363 1.3e-15 0.81 -0.19 413 744 4.4e-09 0.02 -0.17 19 97 1.4e-26 0.32 0.60
AA AA Blast score score score labeled by the score score score score labeled by the score labeled b
START END Psi AA Blast 13 235 8.8e-16 1 26 363 1.3e-15 0 413 744 4.4e-09 0
START END AA AA 13 235 26 363 413 744 19 97
START AA 13 2 26 3 413 7 413 9
CHAIN CHAIN D
PDB ID 2omf 4ubp 4ubp
SEQ D NO: 1318 1318 1318 1324

	PDB annotation		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	Compound	PROTEIN S5; CHAIN: E; 30S RIBOSOMAL PROTEIN S6; CHAIN: F; 30S RIBOSOMAL PROTEIN S7; CHAIN: G; 30S RIBOSOMAL PROTEIN S8; CHAIN: H; 30S RIBOSOMAL PROTEIN S9; CHAIN: I; 30S RIBOSOMAL PROTEIN S10; CHAIN: J; 30S RIBOSOMAL PROTEIN S11; CHAIN: K; 30S RIBOSOMAL PROTEIN S12; CHAIN: L; 30S RIBOSOMAL PROTEIN S13; CHAIN: M; 30S RIBOSOMAL PROTEIN S14; CHAIN: N; 30S RIBOSOMAL PROTEIN S15; CHAIN: O; 30S RIBOSOMAL PROTEIN S16; CHAIN: P; 30S RIBOSOMAL PROTEIN S17; CHAIN: Q; 30S RIBOSOMAL PROTEIN S18; CHAIN: R; 30S RIBOSOMAL PROTEIN S19; CHAIN: S; 30S RIBOSOMAL PROTEIN S20; CHAIN: T; 30S RIBOSOMAL PROTEIN THX; CHAIN: V	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;
Table 5	SEQ FOLD	SCOTE	
Ta.	PMF score		0.95
	Verify score		-0.14
	Psi Blast		0.008
	END		741
	START AA		719
	CHAIN		A
	PDB ID		lalh
	SEQ ID	ÖZ	1325

	PDB annotation												PROTEIN/DNA	HOMEODOMAIN, DNA,	PROTEIN, PROTEIN/DNA	PROTEIN/DNA	COMPLEX DAY DEFINITION	PROTEIN, PROTEIN/DNA	PROTEIN/DNA HOMEODOMAIN, DNA,	
	Compound		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED	BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT	WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH	DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 1AHD 3 REPLACED	BY SEK (C39S) COMPLEX WITH	STRUCTURES) 1AHD 5	HOMEOBOX PROTEIN HOX-B1;	CHAIN: A; PBX1; CHAIN: B; DNA	Chain: D; Dina Chain: E;	HOMEOBOX PROTEIN HOX-B1;	CHAIN: A; PBA1; CHAIN: B; DINA	CHAIN: D; DINA CHAIN: E;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA	
Table 5	SEQ	FULD																		
Tal	PMF	score	0.42		0.78			0.84					0.43			1.00			0.92	
	Verify	score	0.43		0.17			0.19					0.51			0.21			0.51	
	Psi	Blast	1.7e-31		5.1e-32			1.2e-32					5.1e-26			1e-26			1.7e-26	
	END	AA	1075		909			873					1076		- "	909			898	
	START	AA	1015		545			807					1019			549			811	
	CHAIN	a =	d		ď			Ъ					A			A			A	
	PDB	<u> </u>	1ahd		1ahd	•		1ahd		·		-	1b72			1b72			1672	
	SEQ	H Ö			1325			1325	•				1325			1325			1325	

	PDB annotation		COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX; PBX	PROTEIN; DNA BINDING,	HOMEODOMAIN,	DEVELOPMENT, 2	SPECIFICITY	TRANSCRIPTION/DNA	DEOTEIN: DNA BINDING	HOMEODOMAIN.	HOMEOTIC PROTEINS,	DEVELOPMENT, 2	SPECIFICITY	TRANSCRIPTION/DNA	ULTRABITHORAX; PBX	PROTEIN; DNA BINDING,	HOMEODOMAIN,	HOMEOTIC PROTEINS,	DEVELOPMENT, 2	DAIA BRIDAIC BECTERI ICI	UNA-BINDING PROTEIN ISL- 1HD DNA-RINDING	PROTEIN, HOMEODOMAIN,	LIM DOMAIN			
	Compound		CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A;	HOMEOBOX PROTEIN	EXTRADENTICLE; CHAIN: B;	CHAIN: D;	THE PARTY OF THE P	OLIKABITHOKAX HOMEOTIC PROTFIN IV: CHAIN: A:	HOMFOBOX PROTFIN	EXTRADENTICLE; CHAIN: B;	DNA (5'- CHAIN: C; DNA (5'-	CHAIN: D;		ULTRABITHORAX HOMEOTIC	PROTEIN IV; CHAIN: A;	HOMEOBOX PROTEIN	EXTRADENTICLE; CHAIN: B;	DNA (5'- CHAIN: C; DNA (5'-	CHAIN: D;	INSTIT IN GENTE ENITANCED	PROTEIN ISL-1: CHAIN: NULL:			DNA-BINDING PROTEIN ENGPARTED ATTENTOMEDOMARY	LENGTAILED HOMEODOMAIN 1ENH 3	DNA-BINDING PROTEIN
Table 5	SEQ	FOLD							•				,									•					
Ta	PMF	score		0.71				5	1.00						0.75						D 3.4))			86.0		1.00
	Verify	score		0.39				200	75.0						0.54						-0 11	0.11			0.13		0.64
	Psi	Blast		1e-26				12.07	10-71						8.5e-27						4e-19	2			1.7e-18		5.1e-18
	END	AA		1073				203	200						865						1076	>			599		861
	START	AA		1019				540	<u> </u>						811				-		1013)			547		608
	CHAIN	a		¥				<	1,						A												
	PDB	а		1581				158;						;	1681			-			1bw5			,	lenh		1enh
	SEQ	NO E		1325			= **:	1325							1325	·					1325				1325		1325

	PDB annotation		COMPLEX (DNA-BINDING PROTEIN/DNA) DNA- BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA- BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2
	Compound	ENGRAILED HOMEODOMAIN 1ENH 3	PARED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F
Table 5	SEQ FOLD score				:		
Ta	PMF		0.99	1.00	1.00	0.87	0.98
	Verify		0.50	0.15	0.41	0.43	0.19
	Psi Blast		1.7e-24	8.5e-24	1.5e-23	8.5e-24	le-22
	END		1074	604	866	1072	602
	START AA		1015	544	908	1015	545
	CHAIN		A	A	Ą	В	В
	PDB ID		1fj1	1fj1	1fj1	161	1fj1
	SEQ D NO:		1325	1325	1325	1325	1325

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	PDB annotation		REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-	BINDING PROTEIN, DNA,	PAIRED BOX,	I KANSCKIF I I UN Z REGULATION							COMPLEX (ZINC	FINGEK/DNA) ZINC FINGEK, PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)								
	Compound		,	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F		1		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN)	(NMR, 20 STRUCTURES) 1FTZ 3	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN)	(NMR, 20 STRUCTURES) 1FTZ 3	DNA-BINDING FUSHI TARAZU	PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	DNA; CHAIN: A, B, D, E;	CONSENSOS ZINC FINGER PROTEIN; CHAIN: C, F, G;				DNA-BINDING PROTEIN	ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 ISAN 3 REPLACED	BY SER AND RESIDUES 1-6	DELETED (C39S,DEL 1-6) 1SAN 4	(NMK, 20 STRUCTURES) ISAN 3	DNA-BINDING PROTEIN
Table 5	SEQ FOLD	score																								
Ta	PMF			1.00				0.46		99.0		0.57		0.07					9.65							0.99
	Verify			0.40				0.56		0.37		0.27		-0.57					0.91							0.33
	Psi Blast			1.7e-22				5.1e-27		8.5e-27		5.1e-27		3.4e-05					1.4e-28							1./e-29
	END AA	1		864				1073		603		872		223		,		-	1075						707	605
	START	1		807			:	1016		546		808		140					1021						100	155
	CHAIN)		В										၁												
	PDB III)		1£1				1ftz		1ftz		1ftz		1mey					1san					_	-	Isan
	SEQ	NO:		1325				1325		1325		1325		1325					1325						1001	1525

	PDB annotation										COMPLEX (TRANSCRIPTION	KEGULATION/DNA) YING- YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRAINSCRIPTION REGULATION/DNA)	TRANSCRIPTION	REGULATION	TRANSCRIPTION	REGULATION, ADRI, ZINC	FINGER, MIMIN			
	Compound		ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT	WITH CYS 39 1SAN 3 REPLACED BY SEP AND PESIDIRS 1.6	DELETED (C39S,DEL 1-6) 1SAN 4	(NMR, 20 STRUCTURES) 1SAN 5	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CIS 39 ISAN 3 KEFLACED BY SER AND RESIDUES 1-6	DELETED (C39S,DEL 1-6) 1SAN 4 (NMR. 20 STRUCTURES) 1SAN 5	YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS F3 INITIATOR ELEMENT DNA;	CHAIN: A, B;					ADR1; CHAIN: NULL;					COMPLEX(TRANSCRIPTION REGULATION/DNA)	TRAMTRACK PROTEIN (TWO	Line Landent in the Pr
Table 5	SEQ	FOLD																							
Ta	PMF	score					0.87				0.12		<u>,</u>					0.03					0.04		
	Verify	score					29.0				-0.20							-0.09				,	-0.16		
	Psi	Blast					6.8e-30				2e-07	•						1e-08					4e-05		
	END	AA					873			.	218							218					222		
	START	ΑA					813		-		139							139					196		
	CHAIN										C												A		
	PDB	<u></u>				,	1san				1ubd							2adr					2drp		
	SEQ	a ÿ					1325				1325							1325					1325		

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	PDB annotation			COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA BINDING	PROTEIN/DNA) DNA	BINDING, COMPLEX (DNA	DINDLING FROI ELIN/DINA)	COMPLEX (DNA BINDING PROTEIN/DNA) DNA	BINDING, COMPLEX (DNA	BINDING PROTEIN/DNA)	COMPLEX (DNA BINDING	PROTEIN/DNA) DNA	BINDING, COMPLEX (DNA	BINDING PROTEIN/DNA)			COMPLEX (DNA-BINDING	PROTEIN/DNA) HD;	HOMEODOMAIN, COMPLEX	(DNA-BINDING	PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) HD;	DNA-BINDING
	Compound		COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			ENGRAILED HOMEODOMAIN;	CHAIN: A, B; DNA (20-MER);	CHAIN: C, D;		ENGRAILED HOMEODOMAIN; CHAIN: A, B; DNA (20-MER);	CHAIN: C, D;		ENGRAILED HOMEODOMAIN;	CHAIN: A, B; DNA (20-MER);	CHAIN: C, D;		ZINC FINGER /DNA\$ BINDING	DOMAIN ZINC FINGER (/NMR\$) 3ZNF 3	ANTENNAPEDIA PROTEIN;	CHAIN: A, B; DNA; CHAIN: C, D,	Ę, Ę,			ANTENNAPEDIA PROTEIN;	CHAIN: A, B; DNA; CHAIN: C, D,	Д, Г;
Table 5	SEQ	FOLD											• • • • •															
Tal	PMF	score		0:30				0.99				96.0			86.0				0.27		0.74					1.00		
	Verify	score		0.14				0.59				0.36			0.56				-0.30		0.47					0.36		
	Psi	Blast		2e-07		•		5.1e-19				1.4e-18			3.4e-18				800.0		5.1e-29					6.8e-30		
	END	AA		218				1071				601			863				1472		1074					604		
	START	AA		139				1016		• ***		546			808				1445		1019					549		
	CHAIN	9		A				В				В			В						A					A		
	PDB	3		2gli				2hdd				2hdd			2hdd				3znf		9ant					9ant		
	SEQ	a ö		1325				1325				1325			1325				1325		1325					1325		

	PDB annotation	PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX	(DNA-BINDING PROTEIN/DNA)	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE,	REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL	REPEAT, ANK REPEAT	COMPLEX (TRANSCRIPTION	GABPALPHA; GABPBETA1;	COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-	BINDING, 2 NUCLEAR	PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABBAT PHA: GABBETA1:	COMPLEX (TRANSCRIPTION	REGILIATION/DNA) DNA-	BINDING, 2 NUCLEAR	PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	
	Compound		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;		TUMOR SUPPRESSOR P16INK4A;	CHAIN NOLL,	GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;						GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING beoteni beta 1. Chani b.	FINOIDEIN BEIN I, CLIMIN: B, DNA: CHAIN: D F:	J. 7. 1, 1, 1,				
Table 5	SEQ FOLD score								55.04															
Tat	PMF		1.00		1.00		0.15										09.0							
	Verify		0.46		0.51		-0.12										0.02							
	Psi Blast		1.7e-29		6.8e-18		6e-18		1.2e-41								6.8e-38							
	END AA		866		117	-1	114		152								186			-				
	START AA		811		5		9		-								36							
	CHAIN		A						В								В							
	PDB ID		9ant		1a5e	·	1a5e		1awc								1awc							
	SEQ HO NO		1325		1327		1327		1327	-							1327							

l l							
	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER	TUMOR SUPPRESSOR, TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR, TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,
	Compound	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;
Table 5	SEQ FOLD score					51.63	
Ta	PMF	1.00	0.19	0.41	0.43		-0.08
	Verify score	0.30	0.01	0.38	0.33		0.09
	Psi Blast	1.2e-41	0.0012	0.0037	2.4e-06	3.4e-35	3.4e-35
	END	150	408	408	408	154	189
	START AA	\$	350	346	351	,d	39
	CHAIN	В	¥	∢	A		
	PDB	lawc	1b0x	1b4f	1b4f	1bd8	1bd8
	SEQ No ed	1327	1327	1327	1327	1327	1327

	PDB annotation	
	Compound	
Table 5	SEQ	FOI D
Ta	PMF	arous
	Verify PMF	orone
	Psi	Diset
	END	<
	START	<
	CHAIN	E

	PDB annotation	ANKYRIN MOTIF	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6;	P16INK4A, MTS1; CYCLIN	DEPENDENT KINASE,	CYCLIN DEFENDENT KINASE INHIBITORY 2	PROTEIN, CDK, INK4, CELL	CYCLE, MULTIPLE TUMOR	SUPPRESSOR, 3 MTS1,	COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	COMPLEX (INHIBITOR	PROTEIN/KINASE)	INHIBITOR PROTEIN,	CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2	CONTROL, ALPHA/BETA,	COMPLEX (INHIBITOR	PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE)	INHIBITOR PROTEIN,	CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2	CONTROL, ALPHA/BETA,	COMPLEX (INHIBITOR	PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR,
	Compound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR	SUPPRESSOR; CHAIN: B;								CYCLIN-DEPENDENT KINASE 6;	CHAIN: A; P19INK4D; CHAIN: B;							CYCLIN-DEPENDENT KINASE 6;	CHAIN: A; P19INK4D; CHAIN: B;							CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;
Table 5	SEQ FOLD score											53.01																54.97
Tal	PMF		1.00		٠															0.05								
	Verify score		0.38																	0.32								
	Psi Blast		8.5e-19									1e-34								1e-34								6.8e-39
	END		117									157								189								163
	START AA		5																	39								-
	CHAIN		В									В								В								A
	PDB ID		1bi7									1blx								1blx								1bu9
	SEQ NO EQ		1327	*					,			1327								1327								1327

		·				
	PDB annotation	P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN-HELIX,
	Compound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;
Table 5	SEQ FOLD score					
Tal	PMF score		0.87	-0.08	1.00	1.00
	Verify score		0.03	0.12	0.43	0.61
	Psi Blast		3.4e-07	6.8e-39	1.7e-34	3.6e-25
	END		99	191	158	117
	START AA		2	36	ۍ	3
	CHAIN		A	A	A	A
	PDB		1bu9	1bu9	1bu9	1d9s
	SEQ NO:		1327	1327	1327	1327

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	PDB annotation	ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	ANK-REPEAT
	Compound		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B- ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL
Table 5	SEQ FOLD score				56.55				
Ta	PMF		1.00	1.00		0.13	1.00	0.84	0.99
	Verify score		0.33	0.38		0.02	0.16	0.02	0.27
	Psi Blast		1.7e-19	5.1e-17	3.4e-38	3.4e-38	1.2e-33	1.7e-38	1.1e-27
	END		123	117	155	190	154	186	114
	START AA		5	5	1	36	8	5	1
	CHAIN		A	A	V	A	¥	D	
	PDB ID		1d9s	1dcq	lihb	1 ihb	1 ihb	1 ikm	1myo
) E E S		1327	1327	1327	1327	1327	1327	1327

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	PDB annotation	MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR
	Compound		MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	EPHRIN TYPE-B RECEPTOR 2; CHAIN: NULL;	P53; CHAIN: A; 53BP2; CHAIN: B;
Table 5	SEQ FOLD	20016	54.26				53.24
Ta	PMF			1.00	86.0	0.31	
	Verify score			0.35	0.02	-0.31	
	Psi Blast		1.1e-27	1.7e-24	3.4e-38	0.0012	1.2e-22
	END		148	119	186	399	235
	START AA		33	9	5	352	35
	CHAIN				п		В
	PDB ID		lmyo	1myo	1nfi	ISBS	1ycs
	SEQ D SEQ	200	1327	1327	1327	1327	1327

	PDB annotation	PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL
	Compound		P53; CHAIN: A; 53BP2; CHAIN: B;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD				
Ta	PMF		1.00	0.58	90:0
	Verify score		0.20	-0.16	0.02
	Psi Blast		1.7e-20	3.4e-27	5.1e-42
	END AA		93	313	285
	START AA		2	233	201
	CHAIN ID		В	A	U
	PDB ID		lycs	lalh	lmey
	SEQ D G		1327	1330	1330

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	PDB annotation	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN DESIGN 2 CRYSTAI	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		٠			DNA; CHAIN: A, B, D, E;
Table 5	SEQ FOLD score											-						·											
Tat	PMF		1.00	. ,				1.00		•					1.00							1.00							1.00
	Verify score		-0.06					60.0							0.14							-0.11							-0.31
	Psi Blast		1e-45		•			1.5e-46							6.8e-48			•				3.4e-48							1.4e-49
	END		313				-	341							369	*						397							425
	START AA		232					260							288	-				, , , , , , ,		316							344
	CHAIN		ر ت					၁							C							၁							C
	PDB ID		Imey		**			1mey							1mey	`						1mey							1mey
	SEQ NO:		1330	-				1330							1330							1330							1330

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	PDB annotation	FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA INTERACTION, PROTEIN	
	Compound	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	
Table 5	SEQ FOLD score																			100.78										
Tal	PMF					1.00							1.00														1.00			
	Verify score					0.32							09.0														0.52			
	Psi Blast					1e-49							1.2e-50							5.1e-51							5.1e-51			
	END					453							481							482		-					509			
	START AA					372	1						400							400							428			
	CHAIN					3)	•	,				C							C							C			
	PDB ID					1 mev							lmey							1mey					·	-	1mey	,	_	
	SEQ No.					1330						*	1330							1330							1330		_	

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	PDB annotation		DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)
	Compound				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				
Table 5	SEQ FOLD	score																														
Tal	PMF score				1.00		•					1.00							1.00							0.83						
	Verify score			·	0.64							0.19							0.25							0.04						
	Psi Blast				1.5e-50							1.7e-50			- -				5.1e-50							2.4e-37						
	END AA				537						•	593							621							959						
	START AA				456							512							540							540						
	CHAIN ID				C							S			-				S							D D						
	PDB ID				1mey	,		·				lmey	1	-					1mey	,						1mey	•					***
	SEQ ID	NO:			1330							1330							1330							1330						
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Transcript of the state of the	PDB annotation		COMPLEX (ZINC FINGER, DINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S
Table 5	SEQ FOLD	score					-					, A. S.		•																-		
Tak	PMF		1.00		•				0.30						,	0.53								0.92								0.37
	Verify score		0.18						0.13							-0.25								-0.08								-0.50
	Psi Blast		5.1e-50			•	•		1.7e-37							1.7e-32								3.6e-52								3.6e-55
	END AA		649						657				•			350								369								397
	START AA		268						596							202								228		•						239
	CHAIN		ပ						C				-			A								A								A
	PDB		1mey						1mey	,						1#6			_					1tf6				-				1tf6
	SEQ ID	NO:	1330			•			1330							1330								1330								1330

	PDB annotation	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN
	Compound	RIBOSOMAL RNA GENE; CHAIN: R. C. E. F.; C. E. F.; R. P. C. E. F.; P. C. E. F.; P. C. E. F.; P. C. E. F. F. F. F. F. F. F. F. E. E. F.	TFIIIA; CHAÎN: A, D; 5S RIBOSOMAL RNA GENE; CHAÎN: R B, C, E, F; R PP T T	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: R B, C, E, F; R P T T I	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: R C C C R B, C, E, F; R T T
Table 5	SEQ FOLD	21026			
Tat	PMF		0.90	0.54	1.00
	Verify score		-0.57	-0.11	0.16
	Psi Blast		1.7e-36	2.4e-71	1.7e-37
	END AA		406	481	518
	START AA		261	289	373
	CHAIN ID		∀	∢	А
	PDB ID		1116	1tf6	1466
	SEQ D SEQ	OZ.	1330	1330	1330

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	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER
	Compound	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
Table 5	SEQ FOLD score		100.48		
Tal	PMF	1.00		1.00	0.95
	Verify score	0.04		0.17	0.10
	Psi Blast	1.2e-76	3.6e-77	3.6e-77	2.4e-67
	END AA	537	563	593	639
	START AA	373	400	429	457
	CHAIN ID	A	V	A	V
	PDB ID	1116	1466	1476	14f6
	SEQ D NO:	1330	1330	1330	1330

	PDB annotation		PROTEIN	COMPLEX (TRANSCRIPTION REGIT ATTON/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	NITIATION, ZINC FINGER	COLUMN AND ANTOCHER AND ANTOCHE	COMPLEX (I KAINSCRIP IION	KEGULA HON/DINA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGILL ATTON/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-
	Compound			TFIIIA; CHAIN: A, D; 5S RIBOSOMAI, RNA GENE: CHAIN:	B, C, E, F;					() (t : 14:14)	IFIIIA; CHAIN: A, D; 5S	KIBUSUMAL KINA GENE; CHAIIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S RIBOSOMAT RNA GENE: CHAIN:	B.C.E.F.						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;	
Table 5	SEQ FOLD	score																												
Tat	PMF score	2		66.0						6	 	-							0.87							-0.19				
	Verify			0.04							0.00								80.0							0.15				
	Psi Blast			3.4e-37					***	,	le-3/			-					4.8e-47							3.4e-25				
	END	1		631							/59								657							257				
	START			485							513								513							153				
	CHAIN	}		A							А								А							၁				
	PDB	3		1tf6							1446								1tf6							lubd				
	SEQ	i i		1330							1330								1330							1330				

	PDB annotation	PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-	YANG I; IKANSCKIFIJON INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2 FINGER PROTEIN. DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING- VANG 1: TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG I; IKANSCKIF IION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION	יייייי דיייייייייייייייייייייייייייייי
	Compound		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA; CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	CHAIN: A. B:						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	INITIATOR ELEMENT DNA;	CHAIN: A, B;					VVI: CHAIN: C: ADENO-	- ו ו ו אוואווי. לי יוואווי. לי ו ו ו
Table 5	SEQ FOLD score																								
Tal	PMF		0.28					0.70								0.94								77.0	1.74
	Verify score		-0.09					-0.06								-0.27								36.0	-0.2J
	Psi Blast		1.5e-29					3.4e-32								1.1e-53								7 20 51	1.26-31
	END AA		313					341								369								453	453
	START AA		209					235								260								21.4	514
	CHAIN ID		ပ					၁	-							C							-	C	ی
	PDB ID		1ubd					1ubd								1ubd							***	17.7	Inbd
	SEQ D SO SO SO SO SO SO SO SO SO SO SO SO SO		1330					1330								1330									1330

	PDB annotation		REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION INITIATION	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGIT ATTON/DNA) VING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION PEGITI ATTON/DNA) VING	VANG 1: TRANSCRIPTION	INITIATION INITIATOR	ELEMENT, YY1, ZINC 2	
	Compound		ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAN: A B.	(IIAII): A, D,				YY1; CHAIN: C; ADENO-ASSOCIATED VIRIS PS	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YYI; CHAIN: C; ADENO-	INITIATOR ELEMENT DNA:	CHAIN: A B.	CIMIN: A, D,	
Table 5	SEQ	Score																											
Tal	PMF	SCOLE						0.74								1.00									1.00				
	Verify	SCOLE						-0.31								-0.02									0.20				
	Psi Dlact	Diast						1.7e-33								8.5e-35									9.6e-59				
	END	AA						425								453		•							509				
	START	AA						324								352									398				
	CHAIN							၁								C					-				၁				
	PDB	∃						lubd								1ubd	-								1ubd	•			
	SEQ	∃ ÿ						1330				-				1330									1330				

	PDB annotation	FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
	Compound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD score		80.93		
Tal	PMF			1.00	1.00
	Verify score			0.21	0.21
	Psi Blast		9.6e-59	1e-35	1.1e-57
	END AA		510	509	565
	START AA		402	408	454
	CHAIN		U	U	U
	PDB ID		lubd	1ubd	lubd
	SEQ EQ		1330	1330	1330

	PDB annotation		COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC
	Compound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;
Table 5	SEQ FOLD	score																											
Tat	PMF score		0.86						0.64								,	99.0					1.00					0.84	
	Verify score		-0.04						0.19									-0.24					0.12					-0.10	
	Psi Blast		2.4e-46						1e-34									3.4e-32					2.4e-56					1.2e-65	
	END		646						649							•		340					370					399	
	START AA		510						548									201					234			100		260	
	CHAIN		ن ن		· · · · · ·				S							-		A	2				A					A	
	PDB ID		1ubd						1ubd		•							2gli	,				2gli)				2gli	
	SEQ ID	NO:	ļ						1330									1330					1330					1330	

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	PDB annotation	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEA (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION
	Compound		ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				FORMIN BINDING PROTEIN; CHAIN: A;
Table 5	SEQ FOLD score		89.49																								
Tak	PMF						1.00		•			1.00					0.95					0.77					0.36
	Verify score						0.28					0.44					-0.06					0.20					0.07
	Psi Blast		1.2e-71				1.2e-71					8.4e-76					3.6e-63					5.1e-34					0.0011
	END AA		483				483					267					646					651					96
	START AA		344				344					428					484					520					70
	CHAIN ID		A				A					A					A					A					A
	PDB ID		2gli	-			2gli)				2gli					2gli)				2gli)				1e01
	SEQ B G		1330				1330				-	1330					1330					1330					1332

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	PDB annotation	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION	PHOSPHOTRANSFERASE
	Compound	WWPROTOTYPE; CHAIN: A;	PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHATIDYLINOSITOL 3-
Table 5	SEQ FOLD score					
Tal	PMF	0.52	0.96	0.89	0.74	1.00
	Verify score	0.11	0.42	0.47	0.23	0.05
	Psi Blast	0.0044	1.7e-18	4.4e-30	2.2e-31	1.7e-18
	END AA	95	1079	1081	1088	1079
	START AA	70	606	912	907	606
	CHAIN	A	∀	∢	В	В
	PDB ID	1e0m	1pbw	1pbw	Ipbw	1pbw
	SEQ ID NO:	 	1332	1332	1332	1332

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	PDB annotation	RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTFIN GAP CDC42 2	PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION	COMPLEX(GTPASE ACTIVATN/PROTO- ONCOGENE) GTPASE- ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO- ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTE	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA),
	Compound	KINASE; CHAIN: A, B;		RHOGAP; CHAIN: NULL;	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;
Table 5	SEQ FOLD score						
Tal	PMF			1.00	1.00	0.41	0.42
	Verify score			0.33	0.35	0.22	0.10
	Psi Blast			3.4e-43	3.46-44	1.4e-07	1.7e-08
	END			1086	1086	148	129
	START AA			888	891	46	48
	CHAIN				A	Ą	A
	PDB ID			1rgp	1tx4	1a9n	1a9n
	SEQ ID NO:		700	1332	1332	1333	1333

WO 03/029271 PCT/US02/30474 747

	PDB annotation	RNA, SNRNP,RIBONUCLEOPROTE IN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA.	SNRNP, RIBONUCLEOPROTE IN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NIICLEAR PROTEIN/RNA)	RNA,	SNRNP, RIBONUCLEOPROTE IN	CELL ADHESION LEUCINE	BINDING, CELL ADHESION	CELL ADHESION LEUCINE	BINDING, CELL ADHESION	CELL ADHESION LEUCINE	RICH REPEAT, CALCIUM RICH REPEAT, CALCIUM	TRANSFERASE CRYSTAL	STRUCTURE, RAB GERANYLGERANYLTRANSF	ERASE, 2.0 A 2	RESOLUTION, N-	ALPHA SUBUNIT, BETA
	Compound		U2 RNA HARPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: R. D.	CALTAIN: D, D,		INTERNALIN B; CHAIN: A;		INTERNALIN B; CHAIN: A;		INTERNALIN B; CHAIN: A;		RAB	GERANYLGERANYLTRANSFER ASE ALPHA SUBUNIT; CHAIN:	A, C; RAB	GERANYLGERANYLTRANSFER	D;
Table 5	SEQ FOLD score																	
Tak	PMF		0.46		0.34			1.00		0.52		1.00		69.0				
	Verify score		0.05		0.16			0.35		0.14		0.63		0.31				
	Psi Blast		1.4e-07		1.7e-08			5.1e-17		1.7e-08		1.5e-19		5.1e-11				
	END		148		129	•		188		217		144		127				
	START		46		48			42		99		7		35				
	CHAIN ID		O		၁			A		A		A		A	4			
	PDB ID		1a9n		la9n			1d0b		1d0b	,	1d0b		1dce				
	SEQ ID NO:		1333		1333			1333		1333		1333		1333				

																			,		 					
	PDB annotation		SUBUNIT	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYI GERANYI TRANSF	ERASE, 2.0 A 2 RESOLITION N-	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA	SUBUNIT	CONTRACTILE PROTEIN	LEUCINE-RICH REPEAT,	BETA-BETA-ALPHA	CILINDER, DINEIN, 2	CHLAM I DOMONAS, FLAGELLA	RNA BINDING PROTEIN TAP	(NFX1);	RIBONUCLEOPROTEIN	(RNP,RBD OR RRM) AND	LEUCINE-RICH-REPEAT 2	(LANK)	TRANSFERASE ATP:DTMP	PHOSPHOTRANSFERASE	CHAPERONE HSP40;	CHAFENOINE, HEAT SHOCK,	FROI EIIN FOLDING, DINAN	VIRUS/VIRAL PROTEIN J	DOMAIN, HPD MOTIF, ANTI-	PARALLEL HAIRPIN OF
	Compound			RAB GERANYLGERANYLTRANSFER ASF AI PHA SI BI INIT: CHAIN:	A, C; RAB GERANYI GERANYI TRANSFER	ASE BETA SUBUNIT; CHAIN: B, D;		OUTER ARM DYNEIN; CHAIN: A;					NUCLEAR RNA EXPORT	FACTOR 1; CHAIN: A, B;					THYMIDYLATE KINASE; CHAIN:	A;	DNAJ; CHAIN: NULL;			LARGE T ANTIGEN; CHAIN: A;		
Table 5	SEQ	score																								
Ta	PMF	score	-	0.22				0.64				-	0.07						0.03		0.64			0.11		
	Verify	SCOIC		0.24				00.00					-0.17						-0.42		0.35			0.14		
	Psi Blact	Didst		5.1e-13				6.8e-14					8.5e-08						0.0084	i	1.7e-30			2e-06		
	END	A'A		172				149					103						1053		68			80		
	START	AA		46				36					41						1025		6			23		
	CHAIN	≘		A				A					В						A					A		_
	PDB	3		1dce		,		1ds9					1fo1		53.41				4tmk		1bq0			l faf		
	SEQ	∃ Š		1333				1333					1333						1334		1337			1337		
																					 		_		_	

WO 03/029271 PCT/US02/30474 749

	PDB annotation	HELICES	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	TRANSFERASE METHYLTRANSFERASE	TRANSFERASE METHYLTRANSFERASE	METHYLTRANSFERASE	METHIONINE\: GLYCINE	METHYLTRANSFERASE	METHYLTRANSFERASE TRANSFERASE	METHYLTRANSFERASE,	RESTRICTION SYSTEM	COMPLEX (ZINC	FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC
	Compound		HUMAN HSP40; CHAIN: NULL;	GLYCINE N- METHYL TRANSFERASE; CHAIN: A, B, C, D;	GLYCINE N- METHYL TRANSFERASE; CHAIN: A, B, C, D;	GLYCINE N-	METHYLIKANSFEKASE; CHAIN: A, B;		ADENINE-N6-DNA-METHVI TP ANSFER A SE TAOI:	CHAIN: A, B;		OGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;		QGSR ZINC FINGER PEPTIDE;	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;
Table 5	SEQ FOLD score																			80.29
Tal	PMF		1.00	90:0-	0.72	0.42			0.47			0.05					0.62			
	Verify score		0.62	0.18	0.35	-0.19			0.14			-0.11					0.51			
	Psi Blast		1e-29	1.7e-15	4.4e-12	1.7e-19			1.7e-09			3.4e-27					6.8e-28			2.4e-43
	END		88	171	210	171			186			273) 				301			415
	START AA		10	55	61	9		-	58			196)				228			333
	CHAIN			A	¥	A			A			A	((¥			А
	PDB ID		1hdj	1d2h	1d2h	1xva			2adm			1215	1				la1h			1a1h
	SEQ D	5	1337	1339	1339	1339			1339			1349	<u> </u>				1349			1349

WO 03/029271 PCT/US02/30474 750

	PDB annotation		FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA			
	Compound		CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	CRP1; CHAIN: A;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOI D	score						60.74	
Tal	PMF	21006		1.00	1.00	0.99	66.0		0.98
	Verify	SCOIG SCOIG		0.09	0.01	0.24	0.54		0.18
	Psi	Diast		2.4e-43	8.5e-32	9.6e-28	1.7e-22	6e-17	3.4e-46
	END	A.A.		441	441	445	446	439	301
	START	AA		361	361	389	389	245	223
	CHAIN			A	A	A	A	A	O
	PDB	 ∃		lalh	lalh	lalh	lalh	1b8t	lmey
	SEQ	9 <u>2</u>		1349	1349	1349	1349	1349	1349

WO 03/029271 PCT/US02/30474 751

	PDB annotation		INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL STRIICTURE COMPLEX	
	Compound						DNA. CHAIN: A B D E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				!	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			
Table 5	SEQ	FOLD						•													104.85												
Tak	PMF	score					1 00	7.00						1.00														1.00					
	Verify	score					070	0.49						0.44							:							0.27					
	Psi	Blast					12.50	1e-20						1.4e-50							3.4e-51							3.4e-51					
	END	AA						529						357							358							385					
	START	AA					070	248						922)						276	•						304					ļ
	CHAIN	А						ت ن						ر ان)						<u>ن</u>)						C)				
	PDB	<u></u>						lmey						1 mev							1mev		•		•			1mev					
	SEQ	A Ş					12.40	1349	•					1340							1340) }						1349	;				

	PDB annotation	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTFIN-DNA	INTERACTION, PROTEIN DESIGN 2 CRYSTAI	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA;	5S GENE; NMR, TFIIIA,	PROTEIN, DNA,	IKANSCKIPTION FACTOR,	SS KINA 2 GENE, DINA	BINDING PROTEIN, ZINC	FINGER, COMPLEA 3 (TRANSCRIPTION
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEEN: CHAIN: C F G:	FROIEIN; CHAIN: C, F, G,		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER				TRANSCRIPTION FACTOR IIIA:	CHAIN: A; 5S RNA GENE;	CHAIN: E, F;					
Table 5	SEQ FOLD score										2											
Tak	PMF		1.00			1.00				-0.19					0.05	3.						
	Verify score		0.32			0.46				0.19					0.00	9.9						
	Psi Blast		6.8e-51			1.7e-35				1.7e-08					1 10 13	1.10-1.1						
	END		441	***************************************		446				98					204	50c						
	START		360			388				58)				100	199						
	CHAIN		၁			S				٣)					¥						
	PDB ID		1mey			1mey				1mev	Committee of the commit				5	CIII						
	SEQ NO.		1349		,	1349				1349					12,0	1549						

	PDB annotation		REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA:	5S GENE; NMR, TFIIIA,	PROTEIN, DNA,	TRANSCRIPTION FACTOR,	DENDARY DENE, DIVA	BINGER COMPLEX 3	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA
	Compound		•	TRANSCRIPTION FACTOR IIIA; CHAIN: A: 5S RNA GENE:	CHAIN: E, F;							TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;
Table 5	SEQ FOLD	score		60.20																								110.06		
Та	PMF											0.89								0.87			-							
	Verify score											0.07								0.18			***							
	Psi Blast			1.1e-13								2.4e-60								1e-35								1.2e-75		
	END			332						,		385								366							2	418		
	START AA			246								226								228								247		
	CHAIN			A							-1	A								A								A		
	PDB UD			145								1tf6								1tf6								1tf6		-
	SEQ EX	: SC		1349								1349							-	1349								1349		

	PDB annotation	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION
		POLY TRAI INITI				
	Compound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
Table 5	SEQ FOLD score					
Tał	PMF		1.00	1.00	0.99	86.0
	Verify score		0.28	0.03	-0.08	0.02
	Psi Blast		1.7e-37	6e-72	5.16-38	1.2e-75
	END		401	413	423	441
	START AA		249	251	277	277
	CHAIN		∢	¥	∢	A
	PDB ID		14f6	146	11.16	1tf6
	SEQ D C		1349	1349	1349	1349

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	PDB annotation	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION PEGIT ATTON/DNA)	MODELLINIMAN
	Compound			TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					
Table 5	SEQ FOLD score																										
Ta	PMF			1.00						0.77									1.00								
	Verify score			0.24						90.0									0.23								
	Psi Blast			5.1e-37						1.2e-22									1.7e-34								
	END	-		443						301									329								
	START AA			305						198									225								
	CHAIN			A						၁				-					၁								
	PDB ID			1tf6						1ubd					•				1ubd	.,					•		
	SEQ ID NO:			1349						1349	-								1349								

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	PDB annotation	A William State of the State of	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG I; IRANSCKIPIION	INTITUTION, INTITUTORY
	Compound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA:	CHAIN: A, B;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;
Table 5	SEQ FOLD	score							93.07																					
Tal	PMF score		1.00															1.00									1.00			
	Verify score		0.33															0.41									0.10			
	Psi Blast		2.4e-42	,		_			1.1e-55									1.1e-55									6.8e-35			
	END		329						358)								357									385	1		
	START AA		228						248)								251							,		284			
	CHAIN		၁						<u></u>)								2)								C)		
	PDB		1ubd					•	111hd									111hd	2					_			111hd) } •	_	
	SEQ ID		1349						1340					-				1349	;								1349) }		

	PDB annotation		ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG I; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	COMPLEX (TRANSCRIPTION
	Compound					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	Chain: A, B;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			
Table 5	SEQ	FOLD																											
Tat	PMF	score				1.00								1.00									1.00						
	Verify	score				0.17								0.12			•						0.03					,	
	Psi	Blast	,			1.2e-55								2.4e-55									1.7e-35						
	END	AA				413								442	!								441						:
	START	ΑA				302								330	2								340						
	CHAIN	<u>a</u>				C)							C)								O)					
	PDB	<u>a</u>				111bd	}		<u> </u>	,				111hd	3								1ubd	}					
	SEQ	A È				1349	\ \ \							1340									1349	3					

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	PDB annotation	REGULATION/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DINA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	חוות הייים בייים בייים בייים הייים ה
	Compound		ZINC FINGER PROTEIN GLII; CHAIN: A: DNA: CHAIN: C. D;			ZINC FINGER PROTEIN GLI1:	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			
Table 5	SEQ FOLD score														103.49														
Tab	PMF score		1.00			1 00)				1.00									1.00					0.99				
	Verify score		0.14			0.25	ì				0.55									0.29					0.10			a	
	Psi Blast		2.4e-43			3 46-34				•	4.8e-57				1.16-71	7, 27:1				1.1e-71					3.6e-56				
	END		331	,		356					359		•		387	ò				415		-			44.5				
	START AA		198			228	077				240		-		248	01.7				276	ì				304	,			
	CHAIN		A			<	τ.				A					ζ				4	4 4				A	4			
	PDB ID		2gli).rl;	1187				2gli				Jali	78 ₁₁				2oli	1,01				20li	ņ			
	SEQ D NO.	j j	1349			1240	1349				1349				13/10	7+01				1349	}				1340	}			

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	PDB annotation	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	HYDROLASE HYDROLASE,	AIDS, POLYPROTEIN, ASPARTYL PROTEASE,	ACID 2 PROTEASE, HYDROXYETHYLENE	ISOS LEKE INHIBITOR, SUBSTRATE 3 ANALOGUE INHIBITOR	HYDROLASE HIV-1 PROTEASE, MUTANT, DIMER, INHIBITOR, OCCUPANCY	TRANSFERASE ATK, AMGX1, BPK; TYROSINE	KINASE, X-LINKED	AGAMMAGLOBULINEMIA,	XLA, BIK, SH3 2 DOMALIN, TRANSFERASE	TRANSFERASE TYROSINE-	PROTEIN KINASE,	TRANSFERASE, SIGNAL TRANSDICTION 2 SH3	COMPLEX (SH3 DOMAIN/VIRAL
	Compound	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	HTV. 1 PROTFASE CHAIN A B.	1114-1114(0.12.02.), CALLERY 1.5, C.)			PEPTIDE INHIBITOR; CHAIN: A, B; HIV-1 PROTEASE (RETROPEPSIN); CHAIN: C, D;	BRUTON'S TYROSINE KINASE; CHAIN: NULL;				HEMOPOIETIC CELL KINASE;	CHAIN: A, B, C, D, E, F;		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN;
Table 5	SEQ FOLD score														
Tab	PMF	1.00	0 11	0.11			0.37	0.82				0.93			0.87
	Verify score	0.29	0 10	-0.10			0.17	0.57				0.33			0.43
	Psi Blast	3.46-34	20000	0.0090			0.00084	le-16				5.1e-16			1e-18
	END	443	770	047			246	340	•			341	!		341
	START AA	312	40	149			149	280			ē	289	}		289
	CHAIN	A		A			S					A	4		A
	PDB ID	2gli		1bdq 			1 daz	1aww				1hii1	1001		1efn
	SEQ EQ	 		1350			1350	1351				1351	1001		1351

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	PDB annotation		ENHANCER) SRC- HOMOLOGY 3 DOMAIN; COMPLEX (SH3	DOMAIN/VIRAL	ENHANCER), PROTO-	TRANSFERASE, TYROSINE-	PROTEIN KINASE,	PHOSPHORYLATION, 3	AIDS, MYRISTYLATION,	GTP-BINDING, ATP-	BINDING, SH3 DOMAIN, 4	SH2 DOMAIN, PPII HELIX,	PXXP MOTIF	SERINE/THREONINE	PROTEIN KINASE	TRANSFERASE,	SERINE/THREONINE-	PROTEIN KINASE, 2 PROTO-	ONCOGENE, ZINC, ATP-	BINDING, PHORBOL-ESTER	BINDING	PHOSPHOTRANSFERASE C-	SRC, P60-SRC; SRC,	TYROSINE KINASE,	PHOSPHORYLATION, SH2,	SH3, 2 PHOSPHOTYROSINE,	PROTO-ONCOGENE,	PHOSPHOTRANSFERASE	TRANSFERASE PROTO- ONCOGENE TYROSINE
	Compound		CHAIN: B, D;											RAF-1; CHAIN: NULL;								TYROSINE-PROTEIN KINASE	SRC; CHAIN: NULL;						PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;
Table 5	SEQ	Score				•																							
Tak	PMF	acore												90.0								0.16							69.0
	Verify	score												-0.33								0.33							0.26
	Psi	Blast												1.7e-14								1.2e-26							1.5e-19
	END	A'A		***										152								401							341
	START	AA												103								286							286
	CHAIN	a						-																					А
	PDB	3					•							1 faq	ı	**						1fmk							1fyn
	SEQ	9 g												1351								1351						-	1351

	PDB annotation	KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP- BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PE PTIDE)		SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 IGRI 14	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14	
	Compound		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4
Table 5	SEQ FOLD score			65.01			
Ta	PMF		1.00		0.84	0.05	0.31
	Verify score		-0.17		0.07	-0.06	0.52
	Psi Blast		1.5e-19	2.4e-13	5.1e-20	1.7e-23	3.4e-17
	END		341	345	341	397	348
	START AA		288	133	283	289	282
	CHAIN			A	А	A	
	PDB ID		1gfc	1gri	1gri	1gri	lhsq
	SEQ B G Si		1351	1351	1351	1351	1351

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	PDB annotation	COMPLEX (KINASE/PEPTIDE)	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON	TYROSINE KINASE TYROSINE KINASE- INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	CYTOSKELETON CYTOSKELETON,
	Compound	P56—LCK— TYROSINE KINASE; 1LCK 7 CHAIN: A; 1LCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; 1LCK 14 CHAIN: B; 1LCK 15	C-SRC; CHAIN: C; NL1 (MN7- MN2-MN1-PLPPLP); CHAIN: N;	PROTEIN KINASE C DELTA TYPE; 1PTQ 4	PROTEIN KINASE C DELTA TYPE; 1PTQ 4	ALPHA SPECTRIN; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: NULL;	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	ALPHA II SPECTRIN; CHAIN: A;
Table 5	SEQ FOLD score								
Tak	PMF	0.13	86.0	0.23	-0.20	66:0	86.0	0.30	0.89
	Verify score	0.35	0.44	80.0	60.0	0.08	0.57	0.27	0.19
	Psi Blast	5.1e-22	8.5e-18	3.4e-19	5.1e-11	3.4e-15	2.4e-15	3.4e-26	2.4e-15
	END	401	340	152	209	341	341	401	341
:	START AA	289	288	103	176	286	289		289
	CHAIN ID	A	S					4	А
	PDB ID	11ck	1nlo	1ptq	1ptq	1pwt	lpwt	1qcf	1qkw
	SEQ ID NO:	1351	1351	1351	1351	1351	1351	1351	1351

	PDB annotation	MEMBRANE, SH3 DOMAIN	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE- PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE- BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19		TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE	PHOSPHOTRANSFERASE
	Compound		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE- RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D 1SEM 10	PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	ABL TYROSINE KINASE; CHAIN: NULL;	HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	ADENYLATE KINASE
Table 5	SEQ FOLD	SCOJE						
Tal	PMF score		96:0	0.99	0.94	0.05	1.00	1.00
	Verify score		-0.56	0.27	0.37	90.0	0.44	0.11
	Psi Blast		1.7e-16	8.5e-19	1.5e-19	1.7e-23	5.1e-16	4.8e-22
	END		340	338	341	398	341	357
	START AA		286	289	286	281	289	292
	CHAIN ID		A	⋖	A			
	PDB ID		1qly	lsem	lshf	2abl	4hck	1ak2
	SEQ	:OO	1351	1351	1351	1351	1351	1352

	PDB annotation	ATPV:AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE ATP\:AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE ATP\:AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE ATP\:AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE ATP\:AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE ATP\:AMP
	Compound	ISOENZYME-2; CHAIN: NULL;	ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;	ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;	ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;	ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;	ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;
Table 5	SEQ FOLD score						
Tab	PMF		1.00	1.00	1.00	1.00	1.00
	Verify score		0.11	90:0	90.0	0.49	0.49
	Psi Blast		4.8e-22	1.7e-14	1.7e-14	1.7e-36	1.7e-36
	END AA		357	357	357	232	232
	START AA		292	295	295	47	47
	CHAIN						
	PDB ID		1ak2	1ak2	1ak2	1ak2	1ak2
	SEQ PO PO PO PO PO PO PO PO PO PO PO PO PO		1352	1352	1352	1352	1352

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	PDB annotation		PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE	MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE	ATP\:AMP	PHOSPHOTRANSFERASE,	MONOPHOSPHATE KINASE,	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE	ATP\:AMP	PHOSPHOTRANSFERASE,	MYOKINASE; NUCLEOSIDE	MONOPHOSPHATE KINASE,	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE	ATP\:AMP	PHOSPHOTRANSFERASE,	MYOKINASE; NUCLEOSIDE	MONOPHOSPHATE KINASE,	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE	ATP\:AMP	PHOSPHOTRANSFERASE,	MYOKINASE; NUCLEOSIDE	MONOPHOSPHATE KINASE,	PHOSPHOTRANSFERASE	TRANSFERASE (PHOSPHOTRANSFERASE) ATP\:AMP	
	Compound				ADENYLATE KINASE	ISOENZYME-2; CHAIN: NULL;				ADENYLATE KINASE	ISOENZYME-2; CHAIN: NULL;					ADENYLATE KINASE	ISOENZYME-2; CHAIN: NULL;					ADENYLATE KINASE	ISOENZYME-2; CHAIN: NULL;					ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5	
Table 5	SEQ FOLD	score				•		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,				-				88.15						88.15							
Tak	PMF				1.00					1.00																		1.00	
	Verify	2005			0.55					0.55																		0.51	
	Psi Rlaet	Diasi			2.4e-46					2.4e-46						2.4e-46						2.4e-46						2.4e-21	
	END	¥			233	•				233						237						237						357	
	START	¥			47			-		47						47						47						296	
	CHAIN	3																											
	PDB	a a			1ak2					1ak2						1ak2						1ak2			,			1aky	
	SEQ	 ∋			1352					1352	1					1352						1352						1352	

	PDB annotation		PHOSPHOTRANSFERASE, MYOKINASE; 1AKY 6	AIP:AMP	PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15	TRANSFERASE	(PHOSPHOTRANSFERASE)	ATP\:AMP	MYOKINASE: 1AKY 6	ATP:AMP	PHOSPHOTRANSFERASE,	MYOKINASE 1AKY 15	TRANSFERASE	(PHOSPHOTKANSFEKASE)	AIFCAME	PHOSPHOTRANSFERASE,	MYOKINASE; 1AKY 6	ATP:AMP	PHOSPHOTRANSFERASE,	MYOKINASE 1AKY 15	TRANSFERASE	(PHOSPHOTRANSFERASE)	ATP\:AMP	PHOSPHOTRANSFERASE,	MYOKINASE; 1AKY 6	ATP:AMP	PHOSPHOTRANSFERASE,	MYOKINASE 1AKY 15	TRANSFERASE (PHOSPHOTRANSFERASE)
	Compound				-	ADENYLATE KINASE; 1AKY 4	CHAIN: NÚLL; 1AKY 5						ADENYLATE KINASE; 1AKY 4	CHAIN: NULL; 1AKY 5							ADENYLATE KINASE; 1AKY 4	CHAIN: NULL; 1AKY 5							ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5
Table 5	SEQ	FOLD											85.07								85.07								
Tat	PMF	score				1.00			.,,																				1.00
	Verify	score				0.51	! !																						0.86
	Psi	Blast		-		2.4e-21							1.1e-45								1.1e-45								1.1e-45
	END	AA				357	-)						235								235								233
	START	AA				966	ì			-			48								48								49
	CHAIN	А																											
	PDB	А		-		1alvy	, tury	-	•				1aky		-						lakv								laky
	SEQ	[′] A Ş	5			1352	7001						1352				-				1352								1352

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	PDB annotation	ATP\:AMP PHOSPHOTRANSFERASE, MYOKINASE; 1AKY 6 ATP:AMP	PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15	TRANSFERASE (PHOSPHOTRANSFERASE) ATP: AMP	PHOSPHOTRANSFERASE,	MYOKINASE; 1AKY 6	PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15	TRANSFERASE(PHOSPHOTR	ANSFERASE)	TRANSFERASE(PHOSPHOTR ANSFERASE)	TRANSFERASE(PHOSPHOTR	ANSFERASE)	TRANSFERASE(PHOSPHOTR ANSFERASE)	TRANSFERASE(PHOSPHOTR	ANSFERASE)	TRANSFERASE(PHOSPHOTR	TE ANGEED ASE/DHOSPHOTE	ANSFERASE)	TRANSFERASE(PHOSPHOTR	ANSFERASE)	TRANSFERASE(PHOSPHOTR
	Compound			ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5				ADENYLATE KINASE; CHAIN:	A;		ADENYLATE KINASE; CHAIN:	A;		ADENYLATE KINASE; CHAIN:	A;		A PENINT ATE VINA SE. CHAIN.	ADENTERIE MINASE, CIEMIN.	ì		ADENYLATE KINASE; CHAIN:
Table 5	SEQ FOLD score																				
Tat	PMF			1.00				1.00			1.00			1.00			00	1.00			1.00
	Verify score			0.86				0.05			0.05			0.31			22	16.0			0.41
	Psi Blast			1.1e-45				1.7e-14			1.7e-14			1.2e-21			2	17-97.1			2.4e-46
	END			233				358			358)))		357			i d	72/			228
	START AA			49				294			794	ì		295			1	Ç67.			51
	CHAIN							A			A	1		A	:			V		,	А
	PDB ID		,	laky				1c4v			1047	1		1e4v				le4v			le4v
	SEQ EQ			1352				1352			1352	7001		1352				1352			1352

KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL

URIDYLMONOPHOSPHATE/CYT IDYLMONOPHOSPHATE KINASE; CHAIN: A;

1.00

0.90

1.7e-37

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	PDB annotation	ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)	SIGNALING PROTEIN ARF- LIKE PROTEIN 3, ARL3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN	SIGNALING PROTEIN ARF- LIKE PROTEIN 3, ARL3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN
	Compound	A;	ADENYLATE KINASE; CHAIN: A;	ADENYLATE KINASE; CHAIN: A;	ADENYLATE KINASE; CHAIN: A;	ADP-RIBOSYLATION FACTOR- LIKE PROTEIN 3; CHAIN: A;	ADP-RIBOSYLATION FACTOR- LIKE PROTEIN 3; CHAIN: A;
Table 5	SEQ FOLD score						
Tal	PMF		1.00	1.00	1.00	0.17	0.17
	Verify score		0.41	0.40	0.40	-0.82	-0.82
	Psi Blast		2.4e-46	5.1e-33	5.1e-33	0.0073	0.0073
	END AA		228	232	232	78	78
	START AA	-	51	51	51	51	51
	CHAIN		A	A	A	A	∢
	PDB ID		1e4v	1e4v	1e4v	1fzq	1fzq
	SEQ ID		1352	1352	1352	1352	1352

	PDB annotation	2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE	KINASE UMP/CMP KINASE; NIJCLEOSIDE	MONOPHOSPHATE KINASE,	NMF KINASE, FHOSPHOKYL 2 TRANSFER, TRANSITION	STATE ANALOG COMPLEX,	KINASE UMP/CMP KINASE;	NUCLEOSIDE	MONOPHOSPHATE KINASE,	NMP KINASE, PHOSPHORYL	2 TRANSFER, TRANSITION	STATE ANALOG COMPLEX,	TRANSFERASE	KINASE UMP/CMP KINASE; NUCLEOSIDE	MONOPHOSPHATE KINASE,	NMP KINASE, PHOSPHORYL	CTATE ANA! OF COMPLEY	TRANSFERASE							
	Compound		URIDYLMONOPHOSPHATE/CYT	KINASE; CHAIN: A;			URIDYLMONOPHOSPHATE/CYT	IDYLMONOPHOSPHATE	KINASE; CHAIN: A;					URIDYLMONOPHOSPHATE/CYT IDYLMONOPHOSPHATE	KINASE; CHAIN: A;				TRANSFERASE URIDYLATE	KINASE (E.C.2.7.4)	COMPLEXED WITH ADP AND	AMP 1UKZ 3	TRANSFERASE URIDYLATE	KINASE (E.C.2.7.4)	COMPLEXED WITH ADP AND
Table 5	ं SEQ FOLD score						141.35							141.35											
Tal	PMF		1.00													•			68.0				0.89		
ļ	Verify score		06.0																-0.19				-0.19		
	Psi Blast		1.7e-37				1.7e-37							1.7e-37					1.5e-11				1.5e-11		
	END		232				237							237					357				357		
	START AA		44				44							44					292				292		
	CHAIN ID		A				A							A											
	PDB ID		1419				1af9	<u>_</u>						1qf9					1ukz				lukz		
	SEQ D NO:		1352				1352					-	-	1352					1352				1352		

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444	PDB annotation																									TRANSFERASE ATP:AMP-	PHOSPHOTRANSFERASE,	TRANSFERASE	TRANSFERASE ATP:AMP-	PHOSPHOTRANSFERASE, TRANSFERASE
C	Compound		AMP 1UKZ 3	TRANSFERASE URIDYLATE	KINASE (E.C.2.7.4) COMPI EXED WITH AND AND	AMP 1UKZ 3	TRANSFERASE URIDYLATE	COMPLEXED WITH ADP AND	AMP 1UKZ 3	TRANSFERASE URIDYLATE	KINASE (E.C.2.7.4)	COMPLEXED WITH ADP AND	AMP 1UKZ 3	TRANSFERASE URIDYLATE	KINASE (E.C.2.7.4)	COMPLEXED WITH ADP AND	AMP 1UKZ 3	TRANSFERASE URIDYLATE	KINASE (E.C.2.7.4)	COMPLEXED WITH ADP AND	AMP 1UKZ 3	TRANSFERASE URIDYLATE	KINASE (E.C.2.7.4)	COMPLEXED WITH ADP AND	AMP 1UKZ 3	ADENYLATE KINASE; CHAIN: A,	B;		ADENYLATE KINASE; CHAIN: A,	B;
able 5	FOLD	score		158.82			158.82																,,,							
DAGE	score									1.00				1.00				1.00				1.00				1.00			1.00	
Verify	score									0.91				0.91				92.0				0.76				0.32			0.32	
Dei	Blast			1.2e-37			1.2e-37	1 2 2 2		1.2e-37				1.2e-37				5.1e-35				5.1e-35		•		6.8e-15		\dashv	6.8e-15	
HMD	AA			236			236			236				236				232				232				359			359	
START	AA			. 44			44			44				44				51	•			51				291			291	
CHAIN																			_							A			A	
PNR	0			1ukz			lukz			lukz		•	,	lukz	·			lukz			,	lukz		-		1zak		,	Izak	
SEO) A	NO:		1352			1352			1352				1352	,			1352				1352				1352		0.00	1352	

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	PDB annotation	TRANSFERASE ATP:AMP- PHOSPHOTRANSFERASE,	TRANSFERASE TRANSFERASE ATP:AMP-PHOSPHOTRANSFERASE.	TRANSFERASE PHOSPHOTRANSFERASE	ADK; PHOSPHOTRANSFERASE, ZINC FINGER	PHOSPHOTRANSFERASE ADK;	PHOSPHOTRANSFERASE,	PHOSPHOTRANSFERASE ADK.	PHOSPHOTRANSFERASE,	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE, ZINC FINGER	PHOSPHOTRANSFERASE A D.K.	PHOSPHOTRANSFERASE, ZINC FINGED	PHOSPHOTRANSFERASE	ADK; PHOSPHOTRANSFERASE,	ZINC FINGER
	Compound	ADENYLATE KINASE; CHAIN: A, B;	ADENYLATE KINASE; CHAIN: A, B;	ADENYLATE KINASE; CHAIN:	NOLL;	ADENYLATE KINASE; CHAIN: NULL;		ADENYLATE KINASE; CHAIN: NULL:		ADENYLATE KINASE; CHAIN: NULL:		ADENYLATE KINASE; CHAIN: NULL:		ADENYLATE KINASE; CHAIN:	inout,	TRANSFERASE
Table 5	SEQ FOLD	95.58	95.58					88.98		88.98						86.82
Ta	PMF			1.00		1.00						1.00		1.00		
	Verify score			0.39		0.39						0.53		0.53		
	Psi Blast	8.5e-33	8.5e-33	1.7e-16		1.7e-16		3.4e-36		3.4e-36		3.4e-36		3.4e-36		3.4e-28
í	END	246	246	358		358		236		236		232		232		248
- 1	SIAKI	47	47	294	~	294		51		51		53		53	- · · · <u>· ·</u>	44
THITTIO	CHALIN	A	A													A
מממ	EUB D	1zak	1zak	1zin		Izin		Izm		1zin		lzin		Izin	····	2ak3
טבוט	NO:	1352	1352	1352	7,00	1352		1352		1352		1352		1352		1352

	PDB annotation								*			SIGNAL RECOGNITION FFH;	FFH, SRP, GTPASE, SIGNAL RECOGNITION PARTICLE,	GDP	SIGNAL RECOGNITION FFH; FFH, SRP, GTPASE, SIGNAL	RECOGNITION PARTICLE,	GDF									
	Compound		(PHOSPHOTRANSFERASE) ADENYLATE KINASE	ISOENZYME-3 (GTP: AMP	PHOSPHOTRANSFERASE) 2AK3	3 (E.C.2.7.4.10) 2AK3 4	TRANSFERASE	(PHOSPHOTRANSFERASE)	ISOFNZYME-3 (GTD. AMD	PHOSPHOTRANSFERASE) 2AK3	3 (E.C.2.7.4.10) 2AK3 4	SIGNAL SEQUENCE RECOGNITION PROTEIN EET.	CHAIN: NULL;		SIGNAL SEQUENCE RECOGNITION PROTEIN FFH;	CHAIN: NULL;	TRANSFERASE(PHOSPHOTRANS	FERASE) ADENYLATE KINASE	(E.C.2.7.4.3) 3ADK 4 TRANSEED ASE/DITOCOLINGER 13.13	FERASE PHOSPHOLKANS	(E.C.2.7.4.3) 3ADK 4	TRANSFERASE(PHOSPHOTRANS	FERASE) ADENYLATE KINASE	(E.C.2.7.4.3) 3ADK 4	TRANSFERASE(PHOSPHOTRANS	FERASE) ADENYLATE KINASE
Table 5	SEQ FOLD	score				00,00	86.82														-					
Ta	PMF score										,	-0.15		0.15	0.15		1.00		1.00)		1.00			1.00	
;	Verify score										100	0.04		0.04			0.00		0.00			0.11	•		0.11	
	Psi Blast					3 10 28	07-24.6				12.00	16-08		16-08			2.4e-17		2.4e-17			6.8e-14		602 14	0.06-14	
E G	AA					248	0				163	701		162			358		358		Į,	35/		357		
	AA					44	•				18	2		18			287		287			. 167		201		
CHAIN	E D					A																· .			-	
PNR	A					2ak3	-	<u>.</u>			2ng1	b		2ng1			3adk		3adk		20d1r	Jaun		3adk		
SEO	A 5					1352					1352			1352			1352		1352		1350			1352		

	PDB annotation					LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2	ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL	rkolein	COMPLEX (NUCLEOCAPSID PROTEIN/DNA) MOMULV;
	Compound	TRANSFERASE(PHOSPHOTRANS FERASE) ADENYLATE KINASE	TRANSFERASE(PHOSPHOTRANS FERASE) ADENYLATE KINASE	TRANSFERASE(PHOSPHOTRANS FERASE) ADENYLATE KINASE	TRANSFERASE(PHOSPHOTRANS FERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	A, B, C, D;		ALPHA SPECTRIN; CHAIN: A, B, C;		DNA (5'-D(*AP*CP*GP*CP*C)-3'); CHAIN: A; ZINC FINGER PROTEIN NCP10; CHAIN: B;
Table 5	SEQ FOLD	160.04	160.04			53.18		98.56		
Та	PMF score			1.00	1.00					90.0
	Verify score			0.80	0.80					-0.47
	Psi Blast	5.1e-42	5.1e-42	5.1e-42	5.1e-42	6e-09	0 42 00	0.46-09		0.0012
	END AA	236	236	232	232	291	700	167		42
	START AA	42	42	43	43	06	08	So .		14
	CHAIN					¥	V	:		X
	PDB	3adk	3adk	3adk	3adk	lavI	1cm			la6b
	N B S	1352	1352	1352	1352	1358	1358		-+	1362

	PDB annotation	The second secon	INTERCALATION, NUCLEIC ACID, 2 RETROVIRUS, ZINC FINGER	HYDROLASE HYDROLASE,	AIDS, POLYPROTEIN,	ASPARTYL PROTEASE,	HYDROXYETHYLENE	ISOSTERE INHIBITOR,	SUBSTRATE 3 ANALOGUE	INHIBITOR	HYDROLASE HIV-1	PROTEASE, HYDROLASE	TRANSFERASE HIV-1	REVERSE TRANSCRIPTASE,	AIDS, NON-NUCLEOSIDE	INHIBITOR, 2 DRUG DESIGN		TRANSFERASE HIV-1	REVERSE TRANSCRIPTASE,	AIDS, NON-NUCLEOSIDE	INHIBITOR, 2 DRUG DESIGN		TRANSFERASE HIV-1	REVERSE TRANSCRIPTASE,	AIDS, NON-NUCLEOSIDE	INHIBITOR, 2 DRUG DESIGN		TRANSFERASE/IMMUNE	SYSTEM/DNA HIV-1 RT; HIV-1 RT: HIV, DEVERSE	ALLY TAY, THEY ENDE
	Compound			HIV-1 PROTEASE; CHAIN: A, B;			-			TITE A TOTAL COMMENT	HIV-1 PROTEASE; CHAIN: A, B;	TTTY A TO THE THE ACT	HIV-1 KEVERSE	TRANSCRIPTASE (A-CHAIN);	THE VICE THE VERSE	IRANSCRIPTASE (B-CHAIN);	HIV 1 DEVERSE	TD ANICODIDA OF A COLUMN	IRANSCRIPTASE (A-CHAIN);	CHAIN: A; HIV-1 REVERSE	TRANSCRIPTASE (B-CHAIN);	CHAIN: B;	HIV-1 REVERSE	TRANSCRIPTASE (A-CHAIN);	CHAIN: A; HIV-1 REVERSE	TRANSCRIPTASE (B-CHAIN);	CHAIN: B;	HIV-1 REVERSE	IKANSCKIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSF	
Table 5	SEQ FOLD	score														1												153.92	···	
Te	PMF score			0.47						0.10	0.19	1	00.1				0.48)				,	0.96							
	Verify score			0.30						0.34	t	-0.15	7.5				-0.14		•			6	0.02							
	Psi Blast			3.4e-31			`			3 46-32	2C-21-C	0	·				0		,	•	11		>							
ļ	END AA		,,,	136						136		765	,				613	-		-		613		-			707			
⊢	SIAKI		27	74						42	!	169					172			1		170					1,46			
Territoria	CHAIN			₹						A		A					В					B	1				4	4,		
ממת	rus ID		1100	, por						1bwb		1c0t		144			1c0t				•	1c1c)		•		1001			
CEO	A S		1367	7001						1362		1362					1362					1362					1362			

	PDB annotation		TRANSCRIPTASE,	MET 1841LE, 31C, PROTEIN- DNA 2 COMPLEX DRIES	RESISTANCE, M1841.	TRANSFERASE/IMMUNE 3	TRANSFERASE/IMMINE	SYSTEM/DNA HIV-1 RT;	HIV-1 RT; HIV, REVERSE	MET184H F 3TC PROTEIN	DNA 2 COMPLEX DELLA	RESISTANCE, M184I.	TRANSFERASE/IMMUNE 3	SYSTEM/DNA	TRANSFERASE/IMMUNE	SYSTEM/DNA HIV-1 RT;	HIV-1 RT; HIV, REVERSE	FRANSCRIPTASE,	MET184ILE, 3TC, PROTEIN-	DNA 2 COMPLEX, DRUG	RESISTANCE, M184I,	TRANSFERASE/IMMUNE 3	SYSTEM/DNA	TRANSFERASE/IMMUNE	SYSTEM/DNA HIV-1 RT;	HIV-1 RT; HIV, REVERSE	TRANSCRIPTASE,	MET184ILE, 3TC, PROTEIN-	DNA 2 COMPLEX, DRUG RESISTANCE M1841	יודט זיין יידט אין ואניס אין ואניס אין
	Compound		TRANSCRIPTASE (CHAIN B); T	- X			T	J;	TRANSCRIPTASE (CHAIN B):	r	_		HAIN: T; DNA (5'-			 ;;				χ		HAIN: I; DNA (5'-							CHAIN); CHAIN: L; ANTIBODY D] (HEAVY CHAIN); CHAIN: H; RI	
Table 5	SEQ	score													00.071															
Ta	PMF score					·	1.00																72.0	00						
	Verify score						0.01														-		-0.21	-0.41	ą		-			
	Psi Blast						0								·		•						0	>						
	END AA						787		ı					585	3								613	1						
	START						166					-		166		_							166							
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	CHAIN						A	-	,					В									В		-	•				
200	EDE ED						Ic9r							1c9r									1c9r							
Ç	到日	NO:				0,0	1307						-	1362									1362							

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	PDB annotation		TRANSFERASE/IMMUNE 3	HYDROLASE HIV-1	PROTEASE, MUTANT,	DIMER, INHIBITOR,	UCCUPANCY HVDBOI ASE BNIASE II	NUCLEASE RNASE H,	RIBNUCLEASE H, METAL-	BINDING 2 PROTEIN,	PROTEIN FOLDING	HYDROLASE RNASE H,	NUCLEASE, RNASE H*,	RIBNUCLEASE H, METAL-	BINDING 2 PROTEIN,	PROTEIN FOLDING	HYDROLASE HYDROLASE	HYDROLASE HYDROLASE												
	Compound		DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	PEPTIDE INHIBITOR; CHAIN: A,	B; HIV-1 PROTEASE	(RETROPEPSIN); CHAIN: C, D;	RIBONI ICLEASE HIT CHAIN: A:	CONTRACTOR OF CITATION A,				RIBONUCLEASE HI; CHAIN: A;				TITE AND COME AND COME	HIV-1 PROTEASE; CHAIN: A;	HIV-1 PROTEASE; CHAIN: A;	HYDROLASE(ENDORIBONUCLE	ASE) KIBONUCLEASE H	DOMAIN OF /HIV-1\$ REVERSE TRANSCRIPTASE 1HPH 3	HYDROLASE(ACID PROTFASE)	HIV-1 PROTEASE (TETHERED	DIMER LINKED BY 1HVC 3 GLY-	GLY-SER-SER-GLY)	COMPLEXED WITH A-76928	1HVC 4	HYDROLASE(ACID	PROTEINASE) HUMAN	LIMINOLODEFICIENCY VIRUS
Table 5	SEQ	FOLD				-																								
Ta	PMF	score		0.35			0.89					00.1				0.54	40.0	0.05	0.46			60.0						0.11		
	Verify	score		0.33			0.44				500	0.01				77.0	17.0	-0.03	0.13			-0.04						0.39		
	Psi	Blast		8.5e-31			3.4e-16				74.76	7.46-20			,	8 50 22	1 42 22	1.4e-32	3.4e-22			6.8e-33						1.7e-20		
	END:	AA		136			790				707	*				136	100	107				189					,	136		
Į.	STARI	AA		42			651				651	100				38			950			42						47		
. d. i.i.	CHAIN	a		<u> </u>		**	A	-			V								€									¥.		
000	FUB T	3		ldaz	-		1£21				1401					1261						1hvc					1	ilda <i>t</i>		
CTC	SEC E	a Ö		1362			1362				1362					1362	1362	1367				1362					+	7007		

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	PDB annotation						REVERSE TRANSCRIPTASE		REVERSE TRANSCRIPTASE		COMPLEX (ASPARTYL	PROTEASE/INHIBITOR) HIV-	1 PR; HYDROLASE,	ADS, PEPTIDE, INHIBITOR					NUCLEOTIDYLTRANSFERA	SE HIV-1 RT; 1RTH 6 HIV-1	REVERSE TRANSCRIPTASE 1RTH 15	NUCLEOTIDYLTRANSFERA	SE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15	
	Compound		TYPE 2 (HIV-2) PROTEASE 1IDA 3 COMPLEXED WITH THE	INHIBITOR BILA 1906	CONTAINING THE TIDA 4	DIPEPTIDE ISOSTERE 1IDA 5	MMLV REVERSE	TKANSCKIFTASE; IMML 4 CHAIN: NULL; IMML 5	MMLV REVERSE	TRANSCRIPTASE; 1MML 4 CHAIN: NI II 1 : 1MMI 5	HIV-1 PROTEASE: A CYCLIC	PHE-ILE-VAL PEPTIDOMIMETIC	INHIBITOR; CHAIN: C;		HYDROLASE(ENDORIBONUCLE	ASE) KIBONUCLEASE H (E.C.3.1.26.4) 1RIL 3	HYDROLASE(ENDORIBONUCLE	ASE) KIBONUCLEASE H (E.C.3.1.26.4) 1RIL 3	HIV-1 REVERSE	TRANSCRIPTASE; 1RTH 4	CHAIN: A, B; 1RTH 5	HIV-1 REVERSE	TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	
Table 5	SEQ	FOLD							204.88													152.40		
Ta	PMF	score					1.00				690	,			0.43		1.00		1.00					
	Verify	score					0.70				0.25				0.16		0.36		-0.05					
	Psi	Blast					5.1e-67		5.1e-67		8 5é-30				5.1e-11		4.8e-25		0			0		
	END	AA					392		393		134				784		787		768			692		
	START	AA					150		151		42	1			651		651		166			166		
	CHAIN	A						,			Δ	4,							A			A		
	PDB	А					1mm1		1mml		1mtr				Iril		Iril		1rth			11		
	SEQ	A Š					1362		1362		1362	7021			1362		1362		1362	1		1362		

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	PDB annotation		NUCLEOTIDYLTRANSFERA SE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15	NUCLEOTIDYLTRANSFERA SE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15		NUCLEOTIDYLTRANSFERA SE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15	NUCLEOTIDYLTRANSFERA SE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15	NUCLEOTIDYLTRANSFERA SE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15	NUCLEOTIDYLTRANSFERA SE HIV-1 RT; IVRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15	
	Compound		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	HYDROLASE(ACID PROTEINASE) SIMIAN IMMUNODEFICIENCY VIRUS (SIV) PROTEINASE 1SIP 3 (SIV MAC251-32H ISOLATE) (E.C.3.4.23) 1SIP 4	HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	RECORD. /HIV\$-1 PROTEASE
Table 5	SEQ	FOLD	128.83			156.57		125.02		
Tak	PMF	score	•	0.93	0.27		1.00		06.0	0.31
	Verify	score		-0.01	0.38		0.00		-0.05	0.14
	Psi	Blast	0	0	3.4e-21	0	0	0	0	1e-32
	END	AA	602	613	136	712	765	583	613	136
	START	AA	168	168	42	169	169	170	170	42
	CHAIN	А	В	В		⋖	A	В	В	
	PDB		1rth	1rth	lsip	lvrt	lvrt	lvrt	lvrt	2hvp
	SEQ	ДŞ	1362	1362	1362	1362	1362	1362	1362	1362

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	PDB annotation					Olary ver in too	FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC	FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC	FINGER/DNA) COMPLEX	(ZINC FINGER/DNA), ZINC	FINGER, DNA-BINDING PROTEIN	SIGNALLING PROTEIN	BINDING PROTEIN,	CYTOKINE, SIGNALLING	PROTEIN	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA INTERACTION, PROTEIN
	Compound		2HVP 4	NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	יותיוות מחסימיו סימס מ	QGSK ZINC FINGER FEF 11DE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	OGSR ZINC FINGER PEPTIDE:	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	TUMOR NECROSIS FACTOR	RECEPTOR; CHAIN: A, B;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;
Table 5	SEQ	FOLD		123.43								-												
Tab	PMF	score			0.94	,	۰. ا			0.29				0.36				00.00				0.16		
	Verify	score			-0.15	Į,	0.17			0.27				-0.04				0.30				-0.47		
	Psi	Blast		0	0	,	1e-20			1.7e-27				4.8e-30				0.00072				1.7e-30		
	END	AA		583	613		343			371	1			400				614			•	259		
	START	AA		167	167		263			291	1			293	·			452	<u>.</u>			181		
	CHAIN	A		В	В		Ą			4	4 7			A				A	47			S		
	PDB	<u> </u>		3hvt	3hvt		lalh			1914	n n		,	1911				1ext	Toy			1mev		
	SEQ			1362	1362		1367			1367	2			1367)			1367	1001			1367		

	PDB annotation	DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score					
Tal	PMF		0.29	0.18	0.17	0.64
	Verify score		-0.02	0.21	0.27	0.27
	Psi Blast		1.7e-37	3.4e-41	1e-44	1.2e-45
	END		287	315	343	371
	START AA		210	237	262	290
	CHAIN ID		U	U	U	O
	PDB ID		Imey	Imey	1mey	lmey
	SEQ NO:		1367	1367	1367	1367

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	PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER, PROTEIN-DNA
	Compound	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score																				
Tal	PMF	0.21		0.90				1.00					1.00							1.00	
	Verify score	0.01		0.34				0.24					0.63							0.51	
	Psi Blast	3.6e-29		6.8e-47				1e-47					5.1e-48							1.7e-47	
	END AA	399		399	-			427					455							483	
	START AA	290		318				346					374							402	
	CHAIN ID	O		O		•		C)					_	C	,
	PDB ID	lmey		1mey				1mey					1mev							1mey	
	S B S			1367				1367					1367		,					1367	

	PDB annotation		INTERACTION, PROTEIN	DESIGN, 2 CRISIAL	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	FKOI EIN-DINA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	
	Compound					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			
Table 5	SEQ	score				102.78																										
Tat	PMF	acore											1.00							1.00							1.00					
	Verify	score											0.93							0.44							0.00					
	Psi	Blast			_	5.1e-48							5.1e-48							5.1e-48							2.4e-41					
	END	AA				484							511							539							995					
	START	AA				402				·			430							458							458					
	CHAIN	a				C							C							C							S					
	PDB	<u> </u>				1mey	,						1mev							1mev							1mey					
	SEQ	A 8				1367							1367	;						1367	:						1367					

	PDB annotation		(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,
	Compound			DNA; CHAÏN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA: CHAIN: A. B. D. E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER
Table 5	SEQ FOLD	score																												
Tat	PMF			1.00					1.00							1.00							1.00							1.00
	Verify score			0.40					0.52							0.25							0.47							0.58
	Psi Blast			5.1e-46		•			1 7e-46							3.4e-49							1.7e-49							3.4e-50
	END			995					623							650							829							902
	START AA			486					542	!						569							597		•					625
	CHAIN ID			O					ر)						J							C							S
	PDB ID			1mey (1 mev							1mey	`						1mey							1mey
	SEQ	NO:		1367				· · · · · ·	1367							1367					•		1367						•	1367

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	PDB annotation		PROTEIN-DNA INTERACTION PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN DESIGN 2 CRYSTAL	בייים בייים בייים בייים
	Compound		PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		•5			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		
Table 5	SEQ For D	score																														
Tal	PMF	2000					1.00							1.00	,						1.00							1.00				
	Verify	2005					0.49							0.74							0.71							0.28				
	Psi Blact	Diasi					1.7e-50							3.4e-50							3.4e-50							3.4e-36				
	END	Ę					762							790						,	818							825				
	START	Y Y					681							709							737							765				
	CHAIN	}	,				C							C							C							ပ				
	PDB	∃					1mey	,						1 mey		_					1mey							1mev				
	SEQ	a ö					1367			-				1367							1367							1367				

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	PDB annotation	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	KEGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	FKOI EIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					TFIIIA; CHAIN: A, D; 5S	KIBOSOMAL KNA GENE; CHAIN:	B, C, E, F;					
Table 5	SEQ FOLD score															•				-			•	•					
Ta	PMF		0.12					0.99	*						0.99							0.10	-1						
	Verify		-0.17					0.87							0.87							-0.25							
	Psi Blast	*	80-98.9					3.4e-10							9.6e-13							2.4e-41							
	END		235					995							995							427					•		
	START AA		208					540							540							238							
	CHAIN		G					ڻ ن							r D							Ą							
	PDB ID		1mey	**				1mey					•		lmey			***				1416							
	SEQ EQ EQ		1367					1367		·				ļ	1367							1367							

	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER
	Compound	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
Table 5	SEQ FOLD score				
Ta	PMF	0.28	1.00	1.00	0.51
	Verify score	0.0-	0.32	0.40	-0.26
	Psi Blast	1.4e-34	3.4e-36	1.7e-36	6e-71
	END	408	469	520	594
	START AA	263	319	375	375
, 4, 110	CHAIN	¥	A	A	A
4	EDB ID	11f6	14f6	146	1116
0	NO:	1367	1367	1367	1367

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	PDB annotation		PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGITT ATTON/DNA) RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION
	Compound			TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	В, С, Е, Г;				TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;			
Table 5	SEQ	FOLD		106.93																										
Ta	PMF	score							1.00								1.00								0.98					
	Verify	score							0.30								0.25								0.13					
	Psi	Blast		6e-71					1.7e-36								1.5e-37								3.4e-38					
	END	AA		588					575								289								715					
	START	AA		430					431								543								570					
	CHAIN	UI		A	-			•	A								A								¥					
	PDB	an l	,	1466	-				1tf6	•					•		1tf6		·						1466					
	SEQ	NO:		1367					1367								1367								1367					

	PDB annotation		INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	FOLTMENASE III, 2
	Compound		I		RIBOSOMAL RNA GENE; CHAIN: 1	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN: 1	B, C, E, F;							AL RNA GENE; CHAIN:	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;		
Table 5	SEQ FOLD	score	-																													-
Tak	PMF			1.00								1.00								1.00								1.00				
	Verify			0.13								0.28								0.44								0.43				
	Psi Blast			4.8e-71								9.6e-72								1e-36								2.4e-61				
	END			734								790								820								825				
	START	į		570								626								682								682				
	CHAIN	1		A								A								A								A				
	PDB	3		1tf6								1tf6								1tf6								1tf6				
	SEQ	e ë		1367								1367								1367								1367				

	PDB annotation	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION BITTER ATOD	ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION PEGIII ATTON/DNA) VING.	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION
	Compound		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	Chain: A, B;			YY1; CHAIN: C; ADENO-	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-
Table 5	SEQ FOLD score											•												
Tal	PMF		-0.12				0.70	,							1.00									1.00
	Verify score		0.06				0:30								0.03									0.09
	Psi Blast		5.1e-30				3.4e-32								8.4e-43									6.8e-33
	END		343				399		•						427									427
	START AA		245	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			293								316									326
	CHAIN		O				2					•			S									C
	PDB ID		1ubd				1ubd								lubd									1ubd
	SEQ ID NO:		1367	-			1367								1367									1367

	PDB annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2
	Compound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD score				
Ta	PMF	,	1.00	1.00	1.00
	Verify		0.28	0.19	0.87
	Psi Blast		1.2e-33	9.6e-55	1.7e-33
	END		455	483	511
	START AA		354	372	410
	CHAIN		ن ت	ن ت	O
	PDB		1ubd	1ubd	lubd
	S E S	-	1367	1367	1367

SEQ PDB																								
Table 5 Table 6 Table 6 Table 6 Table 7 Table 6 Table 7 Table 6 Table 7 Table 7 Table 7 Table 7 Table 8 Tabl		PDB annotation	FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGILLATION DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION 3	COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING- VANG 1-TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) YING-	DITTO I, INCIDENTIATION	FIEWERS WATER TO SEE THE STATE OF THE SERVICE AND THE SERVICE	ELEMENI, III, CINC 2	FINGER FROI EIN, DIA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)
Tab CHAIN START END Psi Verify PMF		Compound		YYI; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA:	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	CHAN: A B.	CITAIN: P, D,					
PDB	ble 5	SEQ FOLD score			·																			
PDB CHAIN START END Psi	Ta	PMF		0.95		•		1.00								1.00							•	
PDB CHAIN START END		Verify score		0.03				0.33							6	0.29								
PDB CHAIN START D D AA 1ubd C 428 55 1ubd C 438 55 1ubd C 484 56		Psi Blast		6e-52				1.5e-33							2	9.6e-53								
PDB CHAIN DD DD 11ubd C 11ubd		END		995				539							703	294								
PDB U Iubd O D Multiple O D D D D D D D D D D D D		START		428				438							YOY	484								
		CHAIN		၁				၁								ر								
SEQ DD NO: 1367 1367 1367 1367		PDB	:	lubd				1ubd				4.		•••	11.2	pant								
		S E S		1367				1367		•					1361	130/								

	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGUL ATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR
	Compound	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD score				
Ta	PMF	1.00	1.00	1.00	1.00
	Verify score	0.26	0.23	0.25	0.15
	Psi Blast	1.4e-32	2.4e-55	1e-34	5.1e-35
	END	594	650	650	829
	START AA	494	540	549	577
	CHAIN	O	U	U	Ŋ
_	PDB ID	lubd	1ubd	1ubd	1ubd
	SEQ NO:	1367	1367	1367	1367

																								_						
	PDB annotation	•	ELEMENT, YY1, ZINC 2 FINGER PROTEIN DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENI, YYI, ZINC Z	FINGER FROIEIN, DINA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGIT ATTION ON YING.	VANG 1- TRANSCRIPTION	INITIATION. INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION
	Compound		-				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	ChAIN: A, B;						YY1; CHAIN: C; ADENO-ASSOCIATED VIRIS P5	INITIATOR ELEMENT DNA:	CHAIN: A. B;	×					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			
Table 5	SEQ	FOLD																												
Tal	PMF	score					1.00		٠							1.00								1.00						
	Verify	score					0.29									0.43								0.33						
	Psi	Blast					6e-54									3.4e-35								6e-52						
	END:	AA					90/									734								762						
	START	AA					595									633								651						
	CHAIN	UI .					ပ									ပ								၁						
	PDB T	CII					lubd									1npq								1ubd	,					
	SEQ	∃ Ö.					1367									1367				,,,,,,,				1367						

																												_
	PDB amotation	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1: TRANSCRIPTION	INITIATION, INITIATOR EI EMENT VY1 7INC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC
	Compound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA:	CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;	
Table 5	SEQ FOLD score											-																
Tal	PMF		1.00					1.00									1.00									0.49		
	Verify score		0.56					0.38									0.28									-0.16		
	Psi Blast		3.4e-34					1.1e-53									5.1e-35									1.4e-19		
	END		062					818	•				*****				818									258		
	START AA		989					707									717									119		
	CHAIN		၁					C											-							A		
	PDB ID		1ubd					1ubd (******			1ubd									2gli		
			1367					1367								-+	1367							· · ·		1367		

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		1											7											
	PDB annotation	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC FINGER. COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTFIN/DNA) FIVE.	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	COMPLEY (PNA PRIDRIC	COMPLEA (DINA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-
	Compound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	· · · · · · · · · · · · · · · · · · ·		ZINC FINGER PROTEIN GLII; CHAIN: A: DNA: CHAIN: C. D.			ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;			ZINC EINGED DOCTEIN GI 11.	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;	
Table 5	SEQ FOLD score	-																						
Tal	PMF		0.53			0.21			0.95					1.00			1 00	20:1				1.00		
	Verify score		-0.07			0.23			0.17					0.59			990	2				0.22		
	Psi Blast		1.1e-43			8.5e-32			1.2e-55					1e-32			1 20-68	22-27:1				1.2e-70		
	END		429			398			485					482			513					624		
	START AA		238			262			290					354			375					458		
	CHAIN		A			Ą			A					Ą			V	4				А		
	PDB		2gli			2gli			2gli					2gli			2ali	- Eu				2gli		
	SEQ Signal		1367			1367			1367					1367			1367	5				1367		

	PDB annotation	With the state of	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX	(INHIBITOR/NUCLEASE)	COMPLEX (INHIBITOR/NUCLEASE),
			BINI	CON	FINC	FIN	BIN	CO	PRO	ŽĖ —	EIK	BIN	CON	FIN	FIZ	BIN	CO	PRO	Ž	Ž	BIN	<u> </u>	PRC	Ž	Ž	BIN	CO	宫	38
	Compound		,	ZINC FINGER PROTEIN GL11; CHAIN: A: DNA: CHAIN: C. D:				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				RIBONUCLEASE INHIBITOR;	CHAIN: A, D; ANGIOGENIN;	CHAIN: B, E;
Table 5	SEQ FOLD	score																											
Tak	PMF score			0.92				1.00	•••				1.00				96.0					1.00					06'0		
	Verify score			99.0				0.24					0.27				0.29					0.46					0.10		
	Psi Blast			3.4e-33				3.4e-34					1.2e-71				9.6e-68					le-34					5.1e-41		
	END AA			593				649					802				820					820					750		
	START AA			466				522					542				625					689		٠			322		
	CHAIN			A				A					А				A					Y					A		
	PDB ID			2gli	.,,			2gli				•	2gli		************		2gli)				2gli					1a4y	•	
	SEQ ID	NO:		1367				1367	,				1367				1367					1367					1369		

	PDB annotation	COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROI ASF 2 MOI FCI II AR	RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RLANG)	HYDROLASE 2 MOJ, HYDROLASE 2 MOJ, RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX	(INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3
	Compound		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	
Table 5	SEQ FOLD score		260.73					
Ta	PMF				1.00		1.00	
	Verify score				99:0		0.84	
	Psi Blast		3.4e-60		3.4e-60		2e-78	
	END		865		864		861	
	START AA	,	403		481		558	
	CHAIN		∀		A		A	
	PDB ID		1a4y		la4y		1a4y	
	S e s		1369		1369		1369	

	PDB annotation	REPEATS	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA),	RNA, SNRNP,RIBONUCLEOPROTE IN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA)	RNA, SNRNP,RIBONUCLEOPROTE	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX	RNA,	SNRNP, RIBONUCLEOPROTE	CELL ADHESION LEUCINE	BINDING, CELL ADHESION	CELL ADHESION LEUCINE	KICH KEPEAT, CALCIUM BINDING CELL ADHESION	TRANSFERASE CRYSTAL	STRUCTURE, RAB GERANYLGERANYI TRANSF	ERASE, 2.0 A 2	RESOLUTION, N. FORMYLMETHIONINE	(T) 111 (T)
	Compound		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B. D:			INTERNALIN B; CHAIN: A;		INTERNALIN B; CHAIN: A;		RAB	GEKANYLGERANYLTRANSFER ASE ALPHA SUBUNIT; CHAIN:	A, C; RAB	GERANYLGERANYLTRANSFER ASE BETA SUBUNIT; CHAIN: B,	
Table 5	SEQ FOLD score											***************************************						
Та	PMF		0.37		0.19		0.13			0.24		0.13		-0.12				
	Verify score		0.13		0.40		0.59			0.03		-0.19		90.0				
	Psi Blast		3.4e-07		0.0015		0.0015			6.8e-19	,	1.2e-10		1.4e-11				
	END AA		644		750		750			751	7,0	804		999				
	START AA		531		634		634				710	01/		531				
	CHAIN		∢		V		ن ن			₹		1.70		Ψ.				
444	PDB ID		la9n	0	layn		la9n		5	Idop	1905	0001	-	Idce				
070	NO:	,	1369	13/0	1309		1369			1509	1360		1260	1209				

	PDB annotation		ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSF	ENASE, 2.0 A Z RESOLUTION. N-	FORMYLMETHIONINE,	ALPHA SUBUNIT; BETA SUBUNIT	TRANSFERASE CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSF	ERASE, 2.0 A 2	RESOLUTION, N-	FORMYLMETHIONINE,	ALPHA SUBUNIT, BETA	SUBUNIT	CONTRACTILE PROTEIN	LEUCINE-RICH REPEAT,	BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS,	FLAGELLA	CONTRACTILE PROTEIN	LEUCINE-RICH REPEAT,	BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS,	FLAGELLA	RNA BINDING PROTEIN TAP
	Compound		D;	RAB	GERANYLGERANYLTRANSFER	ASE ALPHA SUBUNIT; CHAIN:	A, C, ICAL	ASE BETA SUBUNIT; CHAIN: B,	Ď;	RAB	GERANYLGERANYLTRANSFER	ASE ALPHA SUBUNIT; CHAIN:	A, C; RAB	GERANYLGERANYLTRANSFER	ASE BETA SUBUNIT; CHAIN: B,	D;		OUTER ARM DYNEIN; CHAIN: A;						OUTER ARM DYNEIN; CHAIN: A;						NUCLEAR RNA EXPORT
Table 5	SEQ	FOLD																												
Ta	PMF	score		0.57						0.22								-0.02						-0.14						90.0
	Verify	score		80.0						6.53								0.03						0.12						-0.22
	Psi	Blast		1e-07			,			3.4e-07								1.7e-08						1e-08						3.4e-06
	END	AA		703						198								751						843						732
	START	AA		602						770								286						700						859
	CHAIN	an a		A						A				•				A				•		A						A
:	PDB	<u>a</u>		1dce						1dce								1ds9						1ds9				-		1fo1
	SEQ	NO.		1369				••		1369								1369						1369						1369

	PDB annotation		(NFX1);	RIBONUCLEOPROTEIN	(KNP, KBD OK KKM) AND LEHCINE-RICH-REPFAT 2	(LRR)	RNA BINDING PROTEIN TAP	(NFX1);	RIBONUCLEOPROTEIN	(RNP, RBD OR RRM) AND	LEUCINE-RICH-REPEAT'2	(LRR)	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45;	CYCLIN A/CDK2-	ASSOCIATED PROTEIN P19;	SKP1, SKP2, F-BOX, LRR,	LEUCINE-RICH REPEAT,	SCF. UBIOUITIN. 2 E3.	UBIQUITIN PROTEIN	LIGASE	LIGASE CYCLIN A/CDK2-	CVCI IN A/CDR?-	ASSOCIATED PROTEIN P10.	CKD1 CKD3 F.BOY 1 PP	I PITCHNE DICH DEDEAT	CECCINETICITY 2 EAT,	SCF, UBIQUITIN, 2 E3,	UBIQUITIN PROTEIN	LIGASE	LIGASE CYCLIN A/CDK2-	ASSOCIATED P45; CYCLIN
	Compound		FACTOR 1; CHAIN: A, B;				NUCLEAR RNA EXPORT	FACTOR 1; CHAIN: A, B;					SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L,	N, P,							SKP2; CHAIN: A, C, E, G, I, K, M, O: SKP1. CHAIN: R, D, F, H, T, I	N P.	,,,,							SKP2; CHAIN: A, C; SKP1;	CHAIN: B, D;
Table 5	SEQ	Score																													
Ta	PMF	score					0.30						0.00								-0.18									-0.17	
	Verify	score					-0.16						-0.01								0.00									0.05	
	Psi:	Blast					3.4e-06						1.6e-08								1e-13									1.7e-14	
	END:	AA					732						755	-,							721				•					721	
	START	AA	,				858						434								482									469	
	CHAIN	a					В						A								А									Ą	
	PDB	3					1fo1						1fqv	•							1fqv									1fs2	
	SEQ	a ë					1369		****	·		- 11	1369								1369									1369	

																									_							
	PDB annotation		A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS,	LEUCINE-RICH REPEATS,	SCF, 2 UBIQUITIN, E3,	UBIQUITIN PROTEIN	LIGASE	LIGASE CYCLIN A/CDK2-	ASSOCIATED P45; CYCLIN	A/CDK2-ASSOCIATED P19;	SKF1, SKF2, F-BOX, LKKS,	LEUCINE-KICH KEFEAIS,	SCF, 2 UBIQUITIN, E3,	UBIQUITIN PROTEIN	LIGANE	I KAINSCKIF HOIN KINAIF;	KAINGAF; GIFASE-	ACTIVATING PROTEIN FOR	SPI1, GTPASE-ACTIVATING	PROTEIN, GAP, RNA1P,	RANGAP, LRR, LEUCINE-2	RICH REPEAT PROTEIN,	TWINNING, HEMIHEDRAL	TWINNING, 3 MEROHEDRAL	TWINNING, MEROHEDRY	TRANSCRIPTION RNAIP;	RANGAP; GTPASE-	ACTIVATING PROTEIN FOR	SPII, GTPASE-ACTIVATING	PROTEIN, GAP, RNA1P,	RANGAP, LRR, LEUCINE- 2	RICH REPEAT PROTEIN,
	Compound							SKP2; CHAIN: A, C; SKP1;	CHAIN: B, D;						ration of the strain of the strain of	GIFASE-ACTIVATING FROTEIN	KINAL_SCHPU; CHAIIN: A, B;									GTPASE-ACTIVATING PROTEIN	RNA1_SCHPO; CHAIN: A, B;					
Table 5	SEQ FOLD	score																														
Tal	PMF score							-0.05							ı,	cc.u										68.0						
	Verify score							0.05								0.39									3	0.48						
	Psi Blast							le-13								8.2e-18										8.5e-20						
	END							854							i	10/										846						
	START AA							663								480										552						
	CHAIN ID							¥								¥										А						
	PDB ID							1fs2								lyrg										lyrg						
	SEQ ID	Ö						1369								1369										1369						

	PDB annotation	TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY	TRANSCRIPTION RNAIP; RANGAP; GTPASE- ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP	RICH REPEAT PROTEIN,	I WINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY	ACETYLATION RNASE INHIBITOR,	RIBONUCLEASE/ANGIOGEN	IN INHIBITOR ACETYL ATION LEUCINE.	RICH REPEATS	ACETYLATION RNASE INHIBITOR.	RIBONUCLÉASE/ANGIOGEN	IN INHIBITOR	RICH REPEATS	ACETYLATION RNASE INHIBITOR.	RIBONUCLEASE/ANGIOGEN	IN INHIBITOR	ACETYLATION, LEUCINE- RICH REPEATS
	Compound		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;			RIBONUCLEASE INHIBITOR; CHAIN: NULL:				RIBONUCLEASE INHIBITOR; CHAIN: NUIL:				RIBONUCLEASE INHIBITOR;			
Table 5	SEQ FOLD score									259.80							
Tat	PMF		0.94			96.0								1.00			
	Verify score		0.65			0.21								9.02			
	Psi Blast		5.1e-16			3.4e-47	-			1.5e-65				1.5e-65			
	END AA		862			750		·		865				864			
	START AA		604			322				407				484	-1-		
	CHAIN		Y														
	PDB ID		lyrg		***	2bnh				2bnh				2bnh			
	SEQ ID		1369			1369				1369				1369			

	ηd
	Compound
ole 5	SEO
Tal	PMF
	Verify
	Psi
·	FND
	START
	2

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	PDB annotation		SERINE PROTEASE PCPA2; SERINE PROTEASE, ZYMOGEN, HYDROLASE		HYDROLASE/HYDROLASE INHIBITOR CARBOXYPEPTIDASE A2, LEECH CARBOXYPEPTIDASE	INHIBITOR	HYDROLASE HYDROLASE, CARBOXYPEPTIDASE		ISOMERASE DAP EPIMERASE; METABOLIC ROLE, STRUCTURAL CLASSIFICATION, ISOMERASE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,
	Compound		PROCARBOXYPEPTIDASE A2; CHAIN: NULL;	HYDROLASE (C-TERMINAL PEPTIDASE) CARBOXYPEPTIDASE B (E.C.3.4.12.3) FRACTION II 1CPB	CARBOXYPEPTIDASE A2; CHAIN: A; METALLOCARBOXYPEPTIDASE INHIBITOR; CHAIN: B		CAKBOXYPEPTIDASE T; CHAIN: NULL;		DIAMINOPIMELATE EPIMERASE; CHAIN: A;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER
Table 5	SEQ FOLD score										
Tal	PMF		-0.11	-0.02	-0.07	1	0.05		0.21	90.00	1.00
	Verify score		0.00	60.0	0.01		-0.04		-0.22	-0.29	90.0
	Psi Blast		1.7e-27	3.4e-31	3.4e-27		3.4e-24		5.1e-/2	8.5e-25	3.4e-45
	END		110	110	110		109		343	552	198
	START AA	-	4	2	4		2		2/	454	117
	CHAIN				¥				⋖	∀	S
	PDB		laye	1cpb	1 dtd	,	lobr		lbwz	laih	lmey
	SEQ Signal Construction		1384	1384	1384		1384	,	1388	1389	1389

	PDB annotation	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL
	Compound	PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score					
Tal	PMF		1.00	1.00	1.00	1.00
	Verify score		90.0	0.21	0.21	0.24
	Psi Blast		3.6e-47	4.8e-49	8.5e-49	3.4e-49
	END		198	282	282	310 ·
	START AA		117	201	201	229
	CHAIN		O	U	O	၁
	PDB D		1mey	lmey	1mey	lmey
	SEQ No.		1389	1389	1389	1389

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	PDB annotation	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN DESIGN 2 CRYSTAI	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC
	Compound		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;
Table 5	SEQ FOLD score																													
Tal	PMF		1.00						1.00							1.00							0.45							1.00
	Verify score		0.25						0:30				•			0.01							-0.17							0.20
	Psi Blast		1.2e-49						1.7e-50							3.4e-50							3.4e-40							3.4e-50
•	END		338						366							394							114							422
	START		257						285							313							33							341
	CHAIN		C					•	၁							၁							2							C
	PDB ID		1mey						1mey							1mey							1mey							1mey
	(A) (B) (B) (B) (B) (B) (B) (B) (B) (B) (B		1389				-		1389	-11-2-						1389							1389							1389

WO 03/029271 PCT/US02/30474 806

	PDB annotation	FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	SIRUCIURE, CUMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	FKOI EIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN
	Compound	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	FROIEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	
Table 5	SEQ FOLD score																			104.07										
Ta	PMF					1.00							1.00														0.80			
	Verify					0.07							-0.02														-0.08			
	Psi Blast					8.5e-51							1.2e-49							8.5e-51							3.4e-44			
	END					450							478							479							526			
	START AA					369							397							397							425			
	CHAIN	-				၁				-			ر ر							၁							S			
	PDB					lmey				***			lmey							1mey							1mey			
	SEQ NO:	,				1389						,	1389							1389							1389			

WO 03/029271 PCT/US02/30474 807

	PDB annotation	DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
	Compound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score					
Tal	PMF		0.87	1.00	1.00	1.00
	Verify score		-0.07	-0.10	-0.03	-0.08
	Psi Blast		1.7e-44	8.5e-42	1.7e-43	3.6e-45
	END AA		553	142	170	170
	START AA		453	61	68	91
	CHAIN		U	U	ن ن	၁
	PDB ID		lmey	1mey	1mey	1mey
	SEQ ID NO:		1389	1389	1389	1389

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	PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA INTERACTION PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA). RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA)
	Compound	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	D, C, E, F;				TEIIIA: CHAIN: A D. 58	RIBOSOMAL RNA GENE; CHAIN:
Table 5	SEQ FOLD score									111.69							
Ta	PMF	0.90		0.90		69:0										0 78	0.70
	Verify score	0.19		0.19		-0.14										0.17	-0.14
	Psi Blast	1.2e-13		1e-12		8.5e-12				8.4e-79						8 10.70	0.46-79
	END AA	422		422		553				278						282	707
	START AA	395		395		527				117						118	110
	CHAIN	Ð		Ð		<u>ڻ</u>				А						V	t
	PDB ID	Imey		Imey		1mey				1tf6					_	1+fK	TITO
	SEQ D NO:	1389		1389		1389				1389						1380	1202

	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POL YMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION
	Compound	B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S
Table 5	SEQ FOLD score					
Ta	PMF		0.52	0.71	0.74	0.89
	Verify		-0.03	0.05	0.03	-0.30
	Psi Blast		1.7e-37	1.2e-76	6e-76	2.4e-74
	END AA		319	338	366	394
	START		174	174	202	230
	CHAIN		A	A	∢	A
	PDB ID		1476	1tf6	1116	1tf6
	SEQ ID NO:		1389	1389	1389	1389

	PDB annotation	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTFIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN
	Compound	RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
Table 5	SEQ FOLD score				
Ţ	PMF		06.0	86:0	0.93
	Verify score		0.05	-0.21	0.15
	Psi Blast		1.7e-37	1e-37	5.1e-36
	END AA		436	460	488
	START AA		286	314	342
	CHAIN		Α .	Ą	A
	PDB D		11f6	1476	1116
	SEQ NO:		1389	1389	1389

	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER
	Compound	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
Table 5	SEQ FOLD score				
Ta	PMF	0.48	0.39	0.89	1.00
	Verify score	-0.35	-0.31	0.20	0.13
	Psi Blast	3.6e-67	1.5e-32	1.7e-33	8.4e-67
	END	553	536	207	226
	START AA	370		62	71
	CHAIN	A	A	A	A
	PDB	1116	1466	1466	11f6
	SEQ Sign	1389	1389	1389	1389

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	PDB annotation		PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION	INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING- YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YYT, ZINC 2 FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENI, YYI, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION INITIATION
	Compound			TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIKUS PS	MILIATOR ELEMENT DNA;	CALPAIN, A, B,						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ	FOLD													·										
Ta	PMF	score		0.86			0.99						9	1.00									1.00		
	Verify	score		-0.15			80.0						71.0	-0.15									10.0		
	Psi	Blast		7.2e-77			7.2e-59						1 72 50	1.2e-38								,	9.0e-33		
	END	AA		254			254						210	210								200	200		
L	<u></u>	AA		16			143						100	133			-					320	777		
	CHAIN	a		¥		(<u>۔</u>													-		ار			
	PDB	a		IIIo			pgnI	1.11		-,			1,1hd	non								1.,10	nanı		
	SEQ	NO E	000,	1389		1200	1389						1380	50	,			•				1280	7007		

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	PDB annotation		ELEMENT, YY1, ZINC 2	FINGER FROI EIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION
	Compound							YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			
Table 5	SEQ FOLD	score																														
Tal	PMF							98.0									66.0									1.00						
J	Verify score							-0.13									-0.09									-0.45						
	Psi Blast							5.1e-36									6.8e-35									2.4e-55						
	END							366									422									450						
	START AA							265									321									339						
	CHAIN							C									C									2						
	PDB ID							1ubd									1ubd									1ubd						
	SEQ EQ	SO.						1389									1389									1389						

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	PDB annotation		REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-	YANG 1; TRANSCRÍPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION
	Compound			YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					VVI. CHARL C. APENIO	III; CHAIN: C; ADENO-	ASSOCIATED VIKUS PS	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;
	SEQ	FOLD											1								89.76											
	PMF	score		1.00							98.0	0.00																		0.49		
	Verify	score		0.05							-0.15	3																		-0.34		
	Psi	Blast		1.4e-35							1e-77	1								24.55	2.46-22									8.4e-50		
	END	AA		450							142	1								027	C/+							•	765	. 070		
	START	AA	,,,	346							36	· ·								371	1								200	565		
	CHAIN	€		ت							0)	-		-						ر		
	PDB	a	-	pani							1ubd									111144	9								11.2	non I		
	SEQ	Ö.	1,000	1389							1389		-,-							1380	}								1200			
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	PDB annotation	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3
	Compound	CHAIN: A, B;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD				
Tal	PMF		0.60	0.25	0.03
	Verify score		-0.21	-0.29	-0.30
	Psi Blast		1.5e-32	1.7e-29	3.4e-27
	END AA		526	553	114
	START AA		405	433	5
	CHAIN		D D	O	O
	PDB ID		lubd	lubd	lubd
	SEQ E G SE		1389	1389	1389

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	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENI, YYI, ZINCZ FINGED PROTEIN DNA	PROTEIN RECOGNITION. 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (DNA-BINDING	FROIEIN/DINA) FIVE-
	Compound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	INITIATIOR ELEMENT DNA;	CHAIN: A, B;						CHANGER PROTEIN GLII;	CHAIN: A; DINA; CHAIN: C, D;
Table 5	SEQ FOLD score																												
Tal	PMF score		86.0							66.0									0.83					-				0.87	
1	Verify score		-0.01							-0.03									-0.12									-0.09	
	Psi Blast		4.8e-46							3.6e-55									1.7e-31									2.4e-75	
	END		170							198									198									283	
	START AA	٨	99							<i>L</i> 8									26									117	
	CHAIN		2							Э									ပ									A	
	PDB ID		1ubd							1ubd									1ubd									2gli	_
	SEQ NO:		1389							1389									1389									1389	

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	PDB annotation	FINGER, GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC
₹	Compound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
Table 5	SEQ FOLD score			91.28				
Ta	PMF		98.0		0.95	0.93	0.31	0.29
٠.	Verity score		0.13		-0.21	-0.06	-0.33	-0.14
· ·	Psi Blast		4.8e-75	2.4e-75	1.2e-71	8.4e-72	7.2e-71	1e-29
Ę	END AA		312	340	367	452	500	169
FG	SIAKI AA	-	145	201	201	285	313	33
THE PERSON NAMED IN	CHAIN		A	⋖	∢	A	А	A
מתי	PDB		2gli	2gli	2gli	2gli	2gli	2gli
C	NO:		1389	1389	1389	1389	1389	1389

	PDB annotation	FINGER, COMPLEX (DNA BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDIN PROTEIN/DNA) FIVE-	FINGER, COMPLEX (DNA BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDIN	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDIN	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA	BINDING PROTEIN/DNA)	
	Compound		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				
Table 5	SEQ FOLD score														
Ta	PMF score		0.27		0.57				_	0.42				- 12	
	Verify score		-0.24		-0.05					-0.06					
	Psi Blast		1e-31		1.7e-30					2.4e-59					
	END		528		553		••			200					
	START		377		433					62					
	CHAIN START ID AA		A		A					A					
	PDB ID		2gli		2gli)				2gli)				
	Q - ÷		6		6	-				6				_	

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	PDB annotation	FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE- FINGER GLT: GLT. ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	FRO I EIN/DNA) FI VE- FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	COMPLING FROIEIN/DINA)	COMPLEX (DINA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)		MOTOR PROTEIN MOTOR	PROTEIN, ATPASE,	MICROTUBULE	ASSOCIATED	MOTOR PROTEIN MOTOR	PROTEIN, ATPASE,	MICROTUBULE	ASSOCIATED	MOTOR PROTEIN MOTOR	PROTEIN, ATPASE,	MICROTUBULE	ASSUCIATED	CONTRACTILE PROTEIN
	Compound		ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		יייייי ייייייייייייייייייייייייייייייי	CHAIN: A: DNA; CHAIN: C, D;					KINESIN; CHAIN: NULL;			,	KINESIN; CHAIN: NULL;				KINESIN; CHAIN: NULL;				MICROTUBULE MOTOR
Table 5	SEQ FOLD score															97.18												
Tak	PMF		0.27				0.57			9	0.42									1.00				1.00				1.00
	Verify score	:	-0.24				-0.05			, ,	-0.06			8						0.38				0.35				0.19
	Psi Blast		le-31				1.7e-30				2.4e-59					1e-75				1e-75				3.4e-59				1e-38
	END		528				553				700					237				237				237				231
	START AA		377				433				62					-				1								1
	CHAIN ID		A				A				A															_		A
	PDB ID		2gli				2gli	1-1-		1	2gli	,,				1bg2				1bg2				1bg2)			1cz7
	SEQ ID NO:		1389				1389				1389					1391				1391				1391				1391

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	PDB annotation		NCD, CLARET	SEGREGATIONAL PROTEIN;	NCD CRYSTAL STRUCTURE,	MICROTUBULE MOTORS,	KINESIN 2 SUPERFAMILY,	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN	NCD, CLARET	SEGREGATIONAL PROTEIN;	NCD CRYSTAL STRUCTURE,	MICROTUBULE MOTORS,	KINESIN 2 SUPERFAMILY,	CONTRACTILE PROTEIN	MOTOR PROTEIN MOTOR	PROTEIN, CYTOSKELETON	CONTRACTILE PROTEIN	KINESIN, MICROTUBULE-	BASED MOTOR, NCD,	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN	KINESIN, MICROTUBULE-	BASED MOTOR, NCD, CONTRACTILE PROTEIN								
	Compound		PROTEIN NCD; CHAIN: A, B, C,	D;					MICROTUBULE MOTOR	PROTEIN NCD; CHAIN: A, B, C,	D;					KINESIN; CHAIN: A, B;		KINESIN; CHAIN: A, B;		KINESIN; CHAIN: A, B;		KINESIN; CHAIN: A, B;		KINESIN; CHAIN: A, B;		KINESIN MOTOR NCD; CHAIN:	A;			KINESIN MOTOR NCD; CHAIN:	A;	
Table 5	SEQ FOLD	score																				51.11										
Tat	PMF score				,		:		1.00							06.0		09.0		0.47				1.00		1.00				1.00		
	Verify score								0.24							0.08		0.12		-0.24				-0.25		0.11				0.16		
	Psi Blast	•							99-99							1.7e-35		1.8e-37		6.8e-20		6e-31		6e-31		5.1e-39				1e-66		
	END				-				238	-						146		146		261		257		244		231				236		
	START AA								1							1		9		160		161		162		1						
	CHAIN				•				A							A		A		В		В		В		A				A		
	PDB								1cz7							2kin		2kin		2kin		2kin		2kin		2ncd				2ncd		
	SEQ	NO:							1391							1391		1391		1391		1391		1391		1391				1391		

	PDB annotation	CONTRACTILE PROTEIN. CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN				IN: MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	+	OR TRANSCRIPTION INHIBITOR
	Compound	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR
Table 5	SEQ FOLD score	08.69					57.01		
Tal	PMF score		1.00	1.00	0.99	0.82		0.17	09.0
	Verify score		0.20	0.12	-0.01	-0.46		0.20	0.37
	Psi Blast	4e-62	4e-62	3.4e-40	1.2e-29	5.1e-21	1.2e-29	1.7e-53	1.7e-64
	END AA	236	236	233	244	277	282	362	469
	START AA	-	-	6	164	164	164	117	132
	CHAIN ID				В	В	В	A	А
	PDB ID	3kar	3kar	3kar	3kin	3kin	3kin	1erj	1erj
	S a S	1391	1391	1391	1391	1391	1391	1398	1398

	PDB annotation		BETA-PROPELLER	TRANSCRIPTION INHIBITOR BETA-PROPELLER	TRANSCRIPTION INHIBITOR BETA-PROPELLER	COMPLEX (GTP-BINDING/TRANSDUCER)	BETA1, TRANSDUCIN BÉTA	SUBUNIT; GAMMA1, TRANSDUCIN GAMMA	SUBUNIT; COMPLEX (GTP-	BINDING/TRANSDUCER), G	PROTEIN, HETEROTRIMER 2	SIGNAL TRANSDUCTION	COMPLEX (GTP- BINDING/TRANSDUCER)	BETA1, TRANSDUCIN BETA	SUBUNIT; GAMMA1,	TRANSDUCIN GAMMA	SUBUNIT; COMPLEX (GTP-	BINDING/TRANSDUCER), G	PROTEIN, HETEROTRIMER 2	SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDINGER)	BETA1 TRANSDITCH BETA	SUBUNIT: GAMMA1.	TRANSDUCIN GAMMA	SUBUNIT; COMPLEX (GTP-	BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2
	Compound			TRANSCRIPTIONAL REPRESSOR 7 T/P1; CHAIN: A. B. C:	EPRESSOR	CHIMERA; HAIN: B;						6	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B;	GT-GAMMA; CHAIN: G;	-						GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A: GT-BETA: CHAIN: B:					
Table 5	SEQ	FOLD											118.79			•									-	
Tat	PMF	score		1.00	60.0	99.0															0.99					
	Verify	score		0.72	0.30	0.47															89.0					
	Psi	Blast		le-65	1.7e-62	3.4e-57							5.1e-74						-		5.1e-74					
	END	AA		512	599	418							509		•			•	-		509					
	START	AA		195	285	117	•	•					145								185					
	CHAIN	CTT		A	A	В							В								В					
	PDB	a a		1erj	1erj	1got							1 got		_	_		•			lgot					
	SEQ	NO:		1398	1398	1398							1398								1398					

	PDB annotation	SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2	RIBOSOMAL PROTEIN L11- C76, RIBOSOMAL PROTEIN	RIBOSOME RNA-PROTEIN COMPLEX, RNA, RIBOSOME, TRANSLOCATION, 2 THIOSTREPTON	RIBOSOME RNA-PROTEIN COMPLEX, RNA, RIBOSOME, TRANSLOCATION, 2 THIOSTREPTON	RIBOSOME RIBOSOMAL RNA, TERTIARY STRUCTUR,E RNA-PROTEIN INTERACTION, 2 MINOR GROOVE BINDING, ANTIBIOTIC BINDING, RIBOSOME	COMPLEX (ZINC FINGER/DNA) COMPLEX
	Compound		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	L11 RIBOSOMAL PROTEIN; CHAIN: NULL;	RIBOSOMAL PROTEIN L11; CHAIN: A, B; 23S RIBOSOMAL RNA; CHAIN: C, D;	RIBOSOMAL PROTEIN L11; CHAIN: A, B; 23S RIBOSOMAL RNA; CHAIN: C, D;	RIBOSOMAL PROTEIN L11; CHAIN: A, B; 58 NUCLEOTIDE RIBOSOMAL RNA DOMAIN; CHAIN: C, D;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
Table 5	SEQ FOLD	SCOLE						
Tat	PMF		-0.05	0.83	1.00	1.00	0.89	1.00
	Verify score		0.08	-0.22	0.25	0.50	0.20	0.26
	Psi Blast		8.5e-53	1e-26	1.7e-47	1.7e-27	3.4e-24	4.8e-40
	END AA		599	134	133	133	131	484
	START AA		269	09	18	63	63	404
	CHAIN ID		Д		A	В	A	A
	PDB ID		1got	1aci	1mms	1mms	1qa6	lalh
	SEQ EQ	NO.	1398	1401	1401	1401	1401	1404

	PDB annotation	(ZINC FINGER/DNA); ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA				
	Compound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD score							
Ta	PMF score		1.00	0.51	1.00	1.00	1.00	1.00
	Verify		0.27	0.12	0.21	0.64	0.61	0.23
	Psi Blast		5.1e-26	4.8e-33	2.4e-44	1.2e-42	6.8e-31	5.1e-40
	END AA		484	540	625	736	736	204
	START AA		404	432	544	656	656	123
	CHAIN		А	Ą	А	A	A	S
	PDB ID		lalh	lalh	1a1h	lalh	lalh	1mey
	SEQ ID NO:		1404	1404	1404	1404	1404	1404

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	PDB annotation		INTERACTION, PROTEIN DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROIDIN-DIVA	DESIGN 2 COVETAI	STRICTIRE COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	
	Compound					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	FROI EIN; CHAIN: C, F, G;				DNA: CHAIN: A. B. D. E:	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	-		
Table 5	SEQ	score		-																											
Tal	PMF	37005				1.00						1 00)						1.00							1.00				_	
	Verify	21026				0.56						0.26) !						0.32							0.53					
	Psi Blact	Diast				1.4e-41	•					6 8e-43							1.7e-44							1.4e-45					
	END	¥.				232						260	2						288							316					
	START	AA				151	,					170	` ` `						207							235			-		
	CHAIN	∄				C						ر)						C							C					
	PDB	3				1mey						1 most	ınıcy						1mev	`						Imey	`				
	SEQ	3 g				1404						1404	101						1404							1404					

	PDB annotation		(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEY (71NC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,
	Compound			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DAIA CITABL A D D E.	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				'	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER
Table 5	SEQ FOI D	score																												
Tak	PMF	SCOLE		1.00	•				5	00.1						1.00							1.00							1.00
	Verify	aloas		0.53					7.7	0.41						0.41							0.64							0.64
	Psi	Blast		1.1e-45					77	1.2e-44						8.4e-46					-		1.2e-44		•					1.7e-44
	END	A'A		344						400						400							428							428
	START	AA		263					0	319						319							347							347
	CHAIN	3		S						ပ						C							O							၁
	PDB	a		1mey				···········		lmey						1mey	`						1mev	•						1mey
	SEQ	a ÿ		1404	-					1404						1404							1404							1404

	PDB annotation	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL
	Compound	PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
Table 5	SEQ FOLD					
Tal	PMF		1.00	1.00	1.00	1.00
	Verify score		0.29	0.29	0.50	0.49
	Psi Blast		2.4e-43	5.1e-43	3.4e-43	1.7e-42
	END		456	456	484	512
	START AA		375	375	403	431
	CHAIN		O	O	C	U
	PDB ID		Ime j	1mey	1mey	Imey
	S G S			1404	1404	1404

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	PDB annotation	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	SIRUCIUKE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	FROI EIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC
1	Compound		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER BROTTEIM: CHARL CHARL	INOIEM, CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;
Fable 5	SEQ FOLD score							,																				•		
Ta	PMF		66.0		-				1.00						000	0.93							1.00							1.00
	Verify score		-0.10						0.30						0.10	-0.18						1	0.51						, ,	0.26
	Psi Blast		2.4e-36						5.1e-44						ָ ר ר	/.Ze-5/							8.5e-46						į	5.1e-47
	END		540						540						2/0	208	-						268						707	296
	START AA		431						459						450	409							48/						0.10	CIC
	CHAIN		ပ						<u></u>			***	15			 ر			-				ت							
	PDB		1mey				<u></u>		lmey						\dagger	ımey							ımey					-		ımey
	N H S H S S S S S S S S S S S S S S S S		1404						1404			, .			1404	1404						1404	1404		<u> </u>				+	1404

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	PDB annotation	FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	FKO1EIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER	PROTFIN-DNA	INTERACTION PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER.	PROTEIN-DNÁ INTERACTION PROTEIN	INTERCACION, AND ADAM
The second secon	Compound	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	PROTEIN: CHAIN: C F G.					DNA; CHAIN: A, B, D, E;	PROTEIN; CHAIN: C, F, G;	
Table 5	SEQ FOLD score																										
Tal	PMF					1.00						1.00							1.00						0.04		
	Verify score					0.82						0.59							0.58						-0.13		
	Psi Blast					8.5e-48						3.4e-49							6.8e-51						1.7e-37		
	END AA					624						652			•	,			736						148		
	START AA	-				543						571							655						<i>L</i> 9		
	CHAIN					၁						2							၁						၁		
	PDB ID					1mey						1mey							1mey						lmey		
	SEQ NO.					1404						1404							1404						1404		

	PDB annotation		DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PINOTEIN-DINA	INTERACTION, PROTEIN	DESIGN, 2 CKYSI AL	SIRUCIURE, COMPLEX		EINGER/DNA) ZINC FINGER	PROTEIN-DNA	INTER A CTION DE CTEN	INTERACTION, FROIEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	
	Compound				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	FROIEIN; CHAIN: C, F, G;				DNA: CHAIN: A B D E.	CONSENSIS AND ENGED	DROTTEN: CHAIN: C F G:	INCIEMY, CIEMMY, C, 1, C,					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				
Table 5	SEQ	FOLD																	109.39													
Tat	PMF	score	,		1.00	1					1 00	20:1														1.00						
	Verify	score			99.0						0.48	 									ŧ					0.47						٠
	Psi	Blast			3.4e-51						6 80 51	0.00		•					3.4e-51							6.8e-51						
	END	¥¥			764				•		707	761							793							820						
	START	ΑA			683	***					711	/ F1							711							739						
	CHAIN			:	C						,	ر							C							J						
	PDB	<u> </u>			1mey							ішеу							1mey		•		-			1mey	,					
	SEQ	<u>a</u> §			1404	-					707	1404							1404			4.00				1404						

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	PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC	FINGER/DNA) ZINC FINGER,	PROTEIN-DNA	INTERACTION, PROTEIN	DESIGN, 2 CR 131 AL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC	FINGEK/DNA) ZINC FINGEK, DROTEN-DNA	1 1/O 1 D111 - 1110 1 D111
	Compound	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E; CONSENSUS ZINC.FINGER	PROTEIN; CHAIN: C, F, G;				DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					DNA; CHAIN: A, B, D, E;	PROTEIN: CHAIN: CHAINGER	A 100 LLLL, OALL MITT. C, 1, C,
Table 5	SEQ FOLD score																						
Tat	PMF	1.00		1.00					1.00					0.95							1.00		
	Verify score	0.56		0.57					0.45					-0.14							1.17		
	Psi Blast	3.4e-50		1e-49					1.7e-33					1.4e-39	-						1.7e-12		
	END AA	848		876					880					176							928		
	START	797		795					823					95							849		
	CHAIN	U		ပ					ပ					C							Ŋ		
	PDB ID	Imey		1mey					1mey					1mey							1mey	-	
	SEQ NO:	1404	-	1404					1404		,			1404							1404		

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	ion		OTEIN	PLEX	4)		FINGER/DNA) ZINC FINGER,		OTEIN	Ţ	PLEX	4)	COMPLEX (TRANSCRIPTION	<i>?</i>	COMPLEX (TRANSCRIPTION	1), RNA	2		INITIATION, ZINC FINGER		COMPLEX (TRANSCRIPTION	4)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	2		INITIATION, ZINC FINGER		COMPLEX (TRANSCRIPTION	4)	COMPLEX (TRANSCRIPTION REGULATION/DNA). RNA	
	PDB annotation		INTERACTION, PROTEIN DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	(ZINC	IA) ZIN(NA	INTERACTION, PROTEIN	DESIGN, 2 CRYSTAL	STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	(TRANS	REGULATION/DNA)	(TRANS	REGULATION/DNA), RNA	POLYMERASE III, 2	PTION	ZINC		(TRANS	REGULATION/DNA)	(TRANS	ON/DN/	POLYMERASE III, 2	PTION	N, ZINC		(TRANS	REGULATION/DNA)	COMPLEX (TRANSCRIPTI REGULATION/DNA), RNA	:
	PDE		ERACTI SIGN, 2 (UCTUR	AC FING	COMPLEX (ZINC	GER/DN	PROTEIN-DNA	ERACT	SIGN, 2 (UCTUR	NC FING	MPLEX	BULATI	MPLEX	SULATI	YMER	TRANSCRIPTION	TIATION	PROTEIN	MPLEX	GULATI	MPLEX	GULATI	LYMER	TRANSCRIPTION	TIATIO	PROTEIN	MPLEX	GULATI	MPLEX GULATI)
		_	N S	STR		<u> </u>	E E	PRC	Z	DE	STF		[02		8	REC	POI	TR	Ż	PR(_		8	- RE	PO.		Z	PR(2		88	;
	pu					D, E;	FINGER	J, F, G;); 5S	RIBOSOMAL RNA GENE; CHAIN:); 5S	RIBOSOMAL RNA GENE; CHAIN:); 5S	RIBOSOMAL RNA GENE; CHAIN:		
	Compound					N: A, B,	S ZINC	HAIN: (AIN: A, I	L RNA							AIN: A, I	L RNA							AIN: A, 1	L RNA		
						DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;					TFIIIA; CHAIN: A, D; 5S	SOSOMA	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	SOSOMA	B, C, E, F;						TFIIIA; CHAIN: A, D; 5S	SOSOMA	B, C, E, F;	
					-	N	<u>S</u>	PR(E	RE	B, (TEI	- RE	В, (TE		, B	-
Table 5	SEQ FOLD	score																														
Ta	PMF score					1.00					-		0.83								1.00					.,,,,,			1.00		· · · · ·	
	Verify score					1.17							-0.10								60.0								0.11	٠		
	Psi Blast					4.8e-13							1.1e-62								1.1e-68						_		2.4e-72			
	——					4.8							1.1								1.1								2.4			-
	END					928							288								316								344			
	START					849							124								152								180			
	CHAIN ID					ß							A								A								A			
	PDB ID	_				1mey							1tf6								1tf6								1tf6			
	SEÓ	Ö N				1404							1404								1404								1404			

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	PDB annotation	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION
	Compound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A. D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
Table 5	SEQ FOLD score			126.07		
Tal	PMF		1.00		1.00	1.00
	Verify score	,	-0.05		0.16	0.13
	Psi Blast		4.8e-72	4.8e-74	8.5e-35	4.8e-74
	END		372	403	382	400
	START AA		208	235	236	236
	CHAIN ID		∢	¥	Æ	A
	PDB ID		11f6	11f6	1tf6	1tf6
	SEQ EQ		1404	1404	1404	1404

	PDB annotation		REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION	INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEA (INAMOCKIFILOM	REGULATION/DINA), KINA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN CON ON EX (TEN ANICOD INTION)	COMPLEA (I MAINSCRIFTION DECITY ATTONIONA)	COMPLEY (TRANSCRIPTION)	DECIMATION DAY	KEGULATION/DINA), KINA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGULATIONDNA)	
	Compound				TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	D, C, E, F,		,			TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE; CHAIN:	b, C, E, F;					THE CHAPTA P. CO.	IFILIA; CHALIN: A, D; 35 PIPOSOMAI PMA CENE: CHARI.	KIBUSUMAL KINA GENE, CHAIN.	D, C, E, F;						TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	
Table 5	SEQ	FOLD																											
Tal	PMF	score			1.00							06.0								0.80								96.0	
	Verify	score			0.33							-0.11								0.08								0.12	
	Psi	Blast			1.7e-34							2.4e-63							,	5.1e-34					,			6.8e-36	
	END	AA			469							895							i i	2/8								633	
	START	AA			320							376								452					'š			488	
	CHAIN	A			A							A	•							₹								A	
	PDB	<u> </u>			1tf6				•			1tf6							,	I#6								11f6	
	SEQ	A R			1404							1404								1404								1404	

	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION
	Compound	B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S
Table 5	SEQ FOLD score					
Tal	PMF		1.00	1.00	1.00	1.00
	Verify score		0.12	0.17	-0.11	0.20
	Psi Blast		1.7e-36	4.8e-75	4.8e-76	3.4e-39
	END AA		689	708	736	745
	START AA		544	544	572	009
	CHAIN ID		∢	¥	₩ .	A
	PDB ID	·	1116	1tf6	1116	1tf6
	SEQ EQ		1404	1404	1404	1404

	PDB annotation	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POL YMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN
	Compound	RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
Table 5	SEQ FOLD score				
Tal	PMF		1.00	1.00	1.00
	Verify score		0.26	0.37	0.18
	Psi Blast		7.2e-72	1.7e-37	1.2e-71
	END		792	858	876
	START AA		628	712	712
	CHAIN ID		¥	¥	A
	PDB ID		1116	11f6	11f6
	SEQ B B		1404	1404	1404

9 9	PDB annotation		COMPLEX (TRANSCRIPTION REGULATION/DNA)	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION	INITIATION, ZINC FINGER	PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2 FINGER PROTFIN DNA-	C
	Compound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: D, C, E, E.	D, C, E, I.,				TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	B, C, E, F;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;		
Table 5	SEQ FOLD	score																											
Ta	PMF		86.0					0.74							1.00									1.00					
	Verify score		0.23					-0.14							0.18									0.32					
	Psi Blast		1.7e-30					8.5e-31							8.4e-35									6.8e-28					
	END AA		878					246							204	-								232					
	START		892					96							104									126					
	CHAIN	- 	A					A							S									2					
	PDB ID	1	1tf6					1tf6		***					1ubd				•					1ubd					
	SEÓ	NO:						1404							1404			,				·		1404					

	PDB annotation		PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION			INITIATION, INITIATOR	ELEMENI, I I I, ZINC Z	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION			INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION		<u> </u>	INITIATION, INITIATOR	ELEMENŢ, YY1, ZINC 2	EINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION
	Compound			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	MITIATOR ELEMENT DNA;	CHAIN: A, B;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-
Table 5	SEQ FOI D	score																												
Ta	PMF	2002		1.00								1.00									1.00									1.00
	Verify	SCOLO		0.00								0.11									0.27									0.39
	Psi Blast	Diast		2.4e-44								1.1e-47									6e-54									3.6e-54
	END	AA		232								260									316					•				372
	START	AA		128								156									205									261
	CHAIN	3		C								C									C						,			C
	PDB			1ubd								1ubd									1ubd									1ubd
	SEQ	a ö		1404								1404						·			1404									1404

	PDB annotation	REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2
Transition of the state of the	Compound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD score		98.61		
Ta	PMF			1.00	1.00
	Verify			0.39	-0.03
	Psi Blast		3.6e-54	3.4e-31	2.4e-52
	END		401	400	456
	START AA		291	299	345
	CHAIN		ပ	U	O
	PDB ID		1ubd	1 ubd	1ubd
	S e S		1404	1404	1404

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	PDB annotation		FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGIT ATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING- YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION REGULATION/DNA)
	Compound			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA:	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				
Table 5	SEQ	FOLD																										
Tal	PMF	score		0.99								0.53									0.81							
	Verify	score		0.22								-0.05									0.03							
	Psi	Blast		1.5e-29								2.4e-44									1.7e-29							:
	END	ΑA		484		_						541					-				512							
	START	AA		383								401									406							
	CHAIN	А		C								S									၁							
	PDB			1ubd								1ubd									lubd							
	SEQ	ДÖ		1404								1404		-							1404							

	PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR
	Compound	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD score				
Tar	PMF score	66.0	86.0	1.00	1.00
	Verify score	0.12	0.17	0.53	-0.01
	Psi Blast	2.4e-49	6.8e-30	1.5e-31	1.7e-33
	END AA	969	268	965	624
	START AA	457	467	490	523
	CHAIN ID	U	U	U	S
	PDB ID	1ubd	1ubd (1ubd	1ubd
	SEQ NO:		1404	1404	1404

	PDB annotation	ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATOR INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INTIATION INTIATION ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION
	Compound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
Table 5	SEQ FOLD				
Tal	PMF		1.00	1.00	1.00
	Verify score		0.27	0.18	0.24
	Psi Blast		1.1e-55	6.8e-34	8.4e-56
	END		652	652	708
	START AA		542	551	597
	CHAIN ID		O	v	ပ
	PDB ID		lubd	1ubd	1ubd
	SEQ EQ		1404	1404	1404

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	PDB annotation		REGULATION/DNA)	COMPLEX (TRANSCRIPTION	KEGULATION/DINA) I ING-	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION
	Compound			YY1; CHAIN: C; ADENO-	ASSOCIATED VIKUS PS	CHAIN: A. B:						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;
Table 5	SEQ	roll				•																										
Tat	PMF	score		1.00								1.00									1.00									1.00		
	Verify	score		0.36								-0.03									0.34									0.03		
	Psi	Blast		4.8e-56								2.4e-52									6.8e-35									8.5e-35		
	END	AA		737								764									764									792		
	START	AA		625						•		653									663									691		
	CHAIN	≘		C))									C									၁		
	PDB	<u> </u>		1ubd								1ubd					-				lubd									lubd		
	SEQ	<u>3</u> §		1404								1404									1404									1404		

	PDB annotation		INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA- PROTEIN RECOGNITION. 3	
	Compound		CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	CHAIN: A. B:						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			
Table 5	SEQ	FOLD																												
Tal	PMF	score					0.72								1.00									1.00						
	Verify	score				•	-0.35								0.41									0.36						
	Psi	Blast					3.4e-27								1.1e-53									8.5e-35						
	END	AA					176		_ ,//						820						-			848						
	START	AA					70			٠					709									747						
	CHAIN	<u> </u>					C	,							၁									C						
	PDB	<u></u> 日					1ubd		•		•		-	•	lubd									1ubd				•		
	SEQ	<u> </u>					1404								1404									1404						

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	PDB annotation		COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION PEGITI ATTONIONALY VING	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-	YANG 1; TRANSCRIPTION	INITIATION, INITIATOR	ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-	PROTEIN RECOGNITION, 3	COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING
	Compound		•	YY1; CHAIN: C; ADENO-	ASSOCIATED VINOS F3 INITIATOR ELEMENT DNA;	CHAIN: A, B;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					•	ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;				ZINC FINGER PROTEIN GLII;
Table 5	SEQ	FOLD														•															108.67
Tak	PMF	score		1.00								1.00									1.00					1.00					
	Verify	score		0.36								0.26									0.16					0.27					
	Psi	Blast		1.1e-53								3.4e-33									2.4e-57					1.2e-69					1.2e-69
	END	AA		928								928					•				262					346					402
	START	ΑA		765								775				•					123					207					263
	CHAIN	A		၁								၁									A					A					A
	PDB	A		1ubd								1ubd	•								2gli)				2gli)				2gli
	SEQ	A Ö		1404								1404			-						1404					1404					1404

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	PDB annotation		PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-
	Compound		CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL/1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
Table 5	SEQ	FOLD							
Tab	PMF	score		1.00	1.00	0.64	0.94	0.11	1.00
	Verify	score		0.54	0.40	-0.13	0.19	-0.29	0.25
	Psi	Blast		7.2e-69	4.8e-69	2.4e-61	6.8e-29	99-99	8.5e-32
	END	AA		430	458	542	514	979	595
	START	AA		291	319	375	378	431	459
	CHAIN	О		¥.	A	Ą	A	¥	А
	PDB	A		2gli	2gli	2gli	2gli	2gli	2gli
	SEQ	日 <u>ஜ</u>		1404	1404	1404	1404	1404	1404

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	PDB annotation
	Compound
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	PDB annotation		FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	FINGER, CUMPLEA (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-	FINGER GLI; GLI, ZINC	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLT GLT ZINC	דוווין יייין לייין לייין איזטעון ד
	Compound	v.		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLI1; CHAIN: A: DNA: CHAIN: C. D;			ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	
Table 5	SEQ	FOLD															
Tal	PMF	score		1.00	0.99		1.00			96.0			1.00			1.00	
	Verify	score		0.22	0.42		0.26			0.50			0.25			0.20	
	Psi	Blast		1e-34	1.2e-72		4.8e-70			1.2e-33			7.2e-70			1.2e-33	
	END	AA		629	710		766			763			878			847	
	START	AA		543	571		627			635			711			719	
	CHAIN	А		A	A		A			A			A			A	
	PDB	А		2gli	2gli		2gli			2gli	•		2gli			2gli	
	SEQ	日 <u>Ş</u>		1404	1404		1404			1404			1404			1404	

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	PDB annotation	FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI: GLI, ZINC	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (HSP24/HSP70) HSP70, GRPE, MOLECULAR CHAPERONE, NUCLEOTIDE	EXCHANGE 2 FACTOR, COILED-COIL, COMPLEX	(HSP24/HSP70)	ACTIN-BINDING PROTEIN	ACTIN-BINDING PROTEIN,	CALCIUM-BINDING,	STRUCTURAL PROTEIN	CALPONIN HOMOLOGY,	ACTIN BINDING, STRIICTIRAL PROTEIN	STRUCTURAL PROTEIN	CALPONIN HOMOLOGY, ACTIN BINDING,
	Compound		ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		NUCLEOTIDE EXCHANGE FACTOR GRPE; CHAIN: A, B; MOLECULAR CHAPERONE	DNAK; CHAIN: D;		T-FIMBRIN; CHAIN: NULL;			UTROPHIN; CHAIN: A, B;			UTROPHIN; CHAIN: A, B;	
Table 5	SEQ FOLD score								!								
Tab	PMF		1.00		1.00		0.03			0.53			1.00			1.00	
	Verify		0.50		0.30		-0.23			0.47			0.40			0.48	
	Psi Blast		1.5e-33		3.46-28		0.0036			4.4e-27	_		4.4e-33			1.4e-13	
	END AA		875		231		399			1065			1065			1067	
	START		747		95		297			996			996			896	
	CHAIN ID		A		A		A						4	•		A	
	PDB ID		2gli	•	2gli		1dkg			1aoa			1bhd			1bhd	
	SEQ BOS BOS BOS BOS BOS BOS BOS BOS BOS BOS		1404		1404		1411			1417			1417	1		1417	

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	PDB annotation	STRUCTURAL PROTEIN	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN;	FILAMENTOUS ACTIN-	BINDING DOMAIN, CYTOSKELETON	TRANSFERASE	DINUCLEOTIDE-BINDING	MOLIF, FROSFROMBOSTL TRANSFERASE	STRUCTURAL PROTEIN	DYSTROPHIN, MUSCULAR	DYSTROPHY, CALPONIN	HOMOLOGY DOMAIN, 2	ACTIN-BINDING, UTROPHIN	STRUCTURAL PROTEIN	CALPONIN HOMOLOGY	DOMAIN, DOMAIN	SWAPPING, ACTIN BINDING,	2 UTROPHIN, DYSTROPHIN,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN	CALPONIN HOMOLOGY	DOMAIN, DOMAIN	SWAPPING, ACTIN BINDING,	2 UTROPHIN, DYSTROPHIN,	STRUCTURAL PROTEIN	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK;
	Compound		SPECTRIN BETA CHAIN; CHAIN: A;			NICOTINATE	MONONUCLEOTIDE:5,6- CHAIN:	Α,	DYSTROPHIN; CHAIN: A, B, C, D;		,			UTROPHIN ACTIN BINDING	REGION; CHAIN: A, B;					UTROPHIN ACTIN BINDING	REGION; CHAIN: A, B;					BRUTON'S TYROSINE KINASE; CHAIN: A, B;
Table 5	SEQ FOLD score																									
Lat	PMF		1.00			-0.19			1.00					1.00						1.00						0.59
	Verify score		0.56			0.11			0.46					0.29						0.58						-0.07
	Psi Blast		1.7e-21			2.2e-12			3.4e-12					6.6e-31						1.4e-13						1.7e-11
	END		1070			444	•		1066					1065						1067						119
	START		965			127			896					996						896						9
	CHAIN	-	А			A			A					A						Ą						А
	PDB		1bkr			1d0s			1dxx					lqag						1qag						1btk
	SEQ Signal		1417			1417			1417					1417						1417						1418

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	PDB annotation	TRANSFERASE, PH DOMAIN,	BIK MOTIF, ZINC BINDING, X-LINKED 2	AGAMMAGLOBULINEMIA,	TYROSINE-PROTEIN KINASE	SIGNAL TRANSDUCTION PROTEIN	CYTOSKELETON	SIGNALING PROTEIN	DAPP1, PHISH, BAM32;	PLECKS I KIN, 3-	PHOSPHOINOSITIDES,	INOSITOL	TETRAKISPHOSPHATE 2	SIGNAL TRANSDUCTION	PROTEIN, ADAPTOR	PROTEIN	SIGNALING PROTEIN	DAPP1, PHISH, BAM32;	PLECKSTRIN, 3-	PHOSPHOINOSITIDES,	INOSITOL	TETRAKISPHOSPHATE 2	SIGNAL TRANSDUCTION	PROTEIN, ADAPTOR	PROTEIN	SIGNALING PROTEIN ARF1	EXCHANGE FACTOR AND
	Compound					BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	BETA-SPECTRIN; 1DRO 6 CHAIN: NULL; 1DRO 7	DUAL ADAPTOR OF	PHOSPHOTYROSINE AND 3-	CHAIN: A;							DUAL ADAPTOR OF	PHOSPHOTYROSINE AND 3-	CHAIN: A;							GRP1; CHAIN: A;	
Table 5	· SEQ FOLD	aloss																									
Tak	PMF					0.13	68.0	06.0									0.92			.,						0.39	
	Verify score					0.13	-0.13	0.57									0.37									-0.03	
	Psi Blast					8.5e-15	6.8e-11	3.4e-16									3.4e-16									8.5e-17	
	END					115	113	113									113									123	
•	START AA					8	6	7									7									9	
	CHAIN ID							A									A		-							A	
	PDB ID					1btn	1dro	1fao	-								1fb8									1fgy	
	SEQ ID	Ö				1418	1418	1418									1418									1418	

10 10 10 10 10 10 10 10									
Table 5 Table 5		PDB annotation		PH DOMAIN			SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA,
Tab PDB CHAIN START END Psi Verify PMF		Compound			PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105- LEHHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105- LEHHHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	BRUTON'S TYROSINE KINASE; CHAIN: A, B;
PDB	ole 5	SEQ	FOLD	aloos					
PDB CHAIN START END Psi	Tal	PMF	score		0.35	0.66	86.0	0.30	0.27
PDB CHAIN START END		Verify	score		0.34	0.48	0.40	90.0	0.02
PDB CHAIN START Ipls		Psi	Blast		1.1e-18	5.1e-14	5.1e-16	6.6e-23	6.8e-10
PDB CHAIN ID ID Ipls Ipls Iqqg A Iqqg A		END	AA		123	118	114	151	119
PDB ID Ipls Ipls Iqqg Iqqg Ibfk		START	AA		5	7	5	5	9
		CHAIN	<u></u>				Ą	A	⋖
SEQ ID NO: 1418 1418 1418 1418 1419		PDB	<u></u>		1pls	1pls	1qqg	1qqg	1btk
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